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Fig. 1A

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		1							50
HCV-1	1 a	ATGAGCA	CGAAT	CCTAA	ACCTC		מהמממ	א מרכת א	CACCAACCG
HCV-J	lb		-A					TANCGIAN	CACCAACCG
HCG9	10					·C			
BNL1	1 d					G	<u>-</u>		
BNL2	10					G			
CAM1078	16					·G	<u>-</u>		
FR2	1.5					·G	0	<u>y-</u> y	
r K Z	ΤI					G	c	C	
	•		_						
HC-J6	2 2		- <u>V</u>			·G	c	A-A	
HC-J8	Z D		- <u>A</u>			G	c	A - A	<u>7</u>
S83	2°C		-A			G		A - A	T
NE92	2d		-A			G	C	A-A	T
FR4	2f		-A			6	·Ст-	4-4-	T
BNL4	2e		- A						T
ENL5	. 2h		- <u>y</u>					4-A	T
21.23			- 				·C	A-A	T
NZL1	2 -		3 O.T.						
	29		-ACT			G	C	<u>A</u> - <u>A</u>	T
HCV-TR	ac		-ACT			G-C-	0	2-2	NCT
NE48	3C		-ACT	<u>A</u>	C	G		2-2	
NE274	3a		-ACT	A	C 	G	C	A-A	T
NE145	3e		-ACT	A	C			2-2	GT
NE125	3f		-ATT			6-0-		y-y	ACC
						• •	CC	A A	<u>A</u> CC
2.4	4 a					C	_		
Z 1	4 h		_7			G	 C		
GB358	4.0		-A			6	0		
DK13	4.0					G	C		
	40					G	C		
GB809	4 e				-T	G	C		
BNL7	4 K					G	C		
3E95	5a					G	C	A-A	
HK2	6a		-ACT	<u>A</u>	C	6			
FR1	7a		-ACT		C		_	7 7 7	
			1101	Α		G		A-A	YY
VN4	0 -		3 C II	_	_	_	_		
VN13	0.4		-AC1	-A	C	G	C ·	A-A	·T
ANTZ	ag		-ACT			G	C	A	T
VN12	9a		-ACT	- <u>A</u>	c	G	C	a-a	· <u>V</u>
NE 98	10a		-ACT		4			7-7	N
					-+	G	C	W-W	N



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Fig.1B

	3 -	51		cence		100
HCV-1		TCGCCCACAGGAC				
HCV-J	TD	C		C1		
HC-G9		C				
BNLl		CTK-GS				
BNL2		C				
CAM1078		C				
FR2	1f	C	T <u>A</u>		5G- <i></i>	G
HC-J6	2a	<u>A</u>	TT	c	c	C
HC-J8		C				
s83		Č				
		C				
NE92						
FR4						
BNL3		C				
BNL5	2h	C:	T	C1	:C	C
NZL1	3a				A	
HCV-TR	3b	A	T	c	<u>A</u>	
NE 4 8	3с			c		
NE274						
NE145		GA				
NE125		C				
MIIES	-	9		•		
2.4	4 =	CCAT		 7	·C	
		CAT				
21						
GE358		CCAT				
DK13	4 a	CAT	<u>T</u>			
GB809	4 e	CCAT	T	7	C	C
BNL7	4 k	CCAT	T	7	:c	C
BE95	5a			C1	·	C
2230						
HK2	63	AC				
HN2	Ua	AC				
55.1	-	TAT		~	_	
FR1	/a	TAT				
	_				_	
VN4	8а	C			C	
VN13	86					
VN12	9a	AT3	r	C		
NE 98	10a	CG	T <u>-</u>	1C		
		- -		_		



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Fig.1C

HCV-1		101 TTTACTTGTTGCCGCGCAGGGGC		
HCV-J HC-G9 BNL1	1c	C	CG	G
BNL2 CAM1078 FR2	ld 1e	C	CG	G AGC-G
HC-J6 HC-J8	2a 2b	-AC	CG CG	AG
S83 NE92	2c	-AC	G	G
FR4 BNL3	2f	-A	C G	C-AG
BNL5	2 b	-A	CC-G	G
NZL1 HCV-TR	3a	-AG	AC	C-T
NE48	3с	- <u>V</u> G	CT	TAC-T
NE274 NE145	3d 3e	-CAC	A	AGTTC-T
NE125	3f	-AG-A	AC	AGT-C-T
Z4 Z1	4a		cg	TC
GB358	4.C	C		AG-TC-G TG
DK13	4d			TG
GB809 BNL7	4 e 4 k		G- 	TC-G
BE95				
нк2	6a		CC-G	
FR1	7a		C-T	
VN4 VN13	8a 8b	-CC	GC-C	
VN12	9a	-CA	AC-T	G
NE98	10a	GC- <u>Y</u> <u>Y</u>	CCAG	TAGT-C-C



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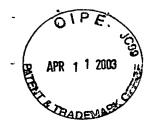
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Fig.1D

HCV-1 HCV-J	1b	200 AAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAA
HC-G9 BNL1	1d	TTTTT
BNL2	_d	T-ACGAT-ACGA
CAM1078	⊥e	GTGGCAT
FR2	ŢŢ	
HC-J6	2a	GCGATAGCCT
HC-J8	2b	TACGGTACCC
S83	2c	A
NE92	2d	A
FR4 BNL3	2I	T-AC-G-A-T-A-G-C-CA
BNT'2	2 e	T-AC-G-A-T-A-G-C-CT
DMED	21:	AACGATGGCT
NZL1	3a	ATAAGCACA
HCV-TR	3b	C-T
NE48	3с	C-CGC-GG
NE274	3d	AAGCCAACC-GG
NE145 NE125	Je	ATT
NEIZJ	31	AT
Z.4	4 a	GA
Z1	4 b	GATCG
GB358	4 C	G
DK13	4 d	
GB809	4 e	G
BNL7	4 K	GTGCA
BE95	5 a	GATAC-GTT
HK2	6 a	ACGCACGCA <u>A</u> <u>A</u>
FR1	7 a	CACGACGCAA
VN4 VN13	8a	T-AC-G-CAG-C-A-A-A-A-AA
*****	O.D	л1МССЧ-ССЧДС
VN12		GACGG-CAGCAAAA
NE98	10a	G



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Fig.1E

HCV-1 HCV-J HC-G9 BNL1 BNL2 CAM1078 FR2	201 250 la GGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGC lb
HC-J6 HC-J8 S83 NE92 FR4 BNL3 BNL5	2aAGCTACTAATGAA-AA-A
NZL1 HCV-TR NE48 NE274 NE145 NE125	3aGAGACT
Z4 Z1 GB358 DK13 GB809 BNL7	4a GC-AA
BE95	5aGC-AACCTGA
нк2	6aGC-ACAAA
FR1	7aTAC-AGACAC-T-GGAC
VN4 VN13	8a A-TGC-AC-AAACC-TC 8bTGAC-AAACC-TA
VN12	9aTGC-A-AA-C-AC-ATT
NE98	10aGCAATT



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Fig.1F

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	1d 1d	251 CCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGATGGCTCCTGTCTCTCTC	A C C
HC-J6 HC-J8 S83 NE92 FR4 BNL3 BNL5	2a 2b 2c 2d 2f 2e	2A-C-GACTCA	C C C C
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	ATCAGCC	
24 21 GB358 DK13 GB809 BNL7	40 40 4d 4e	A	: LT L
BE95	5a	TC-CCTAGGC	T
HK2		-TTAC	
FR1		TCAC	
VN4 VN13	8a 8b	-TTA	
VN12		TGC	
NE98	10a	AG	G



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Fig.1G

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	301 350 La CGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCG lb
HC-J6 HC-J8 S83 NE92 FR4 BNL3 BNL5	2aATCTCTCTATAC 2bCGTCTC
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a CC-T-ATCAATGC- 3b TCTAATAATA-C- 3c C-TGAATA-AA-AA
Z4 Z1 GB358 DK13 GB809 BNL7	4a C
BE95	5aAATATA-AA
HK2	6aCCACATAT
FR1	7aCGTATACAC
VN4 VN13	BaCGC Bb -NCN-GC
VN12	9aN-GNNN-GN-G
NE98	0a C



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Fig.1H

HCV-1 HCV-J HC-G9 FR2	351 400 1a CAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCA 1b T
HC-J6 HC-J8 583 NE92 FR4 BNL3	2a CG
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a
Z4 Z1 GB358 DK13 GB809	4a C
BE95	5a TAT
HK2	6a GTTTT
FR1	7aCA-NNC-A
VN4 VN13	8aC
VN12	9aCC



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Fig.1I

HCV-1	l a	401 TGGGGTACA	TACCGO	ፐርርጥር	GGCGCC	- ርጥርጥጥ	GGAGG	CECTECC	450 A 366CC
HCV-J									
HC-G9									
FR2									
			•				•	-	1171
HC-J6	2 a		-сто	A		GC	C	ТС	<u>Δ</u> π
HC-J8									
S83									
NE92									
FR4									
BNT.3									
51.23			1, 00			00 G	C .	9-1N- ·	
N27.1	Зa		-C	. -		G-A		TCA	2-
HCV-TR									
NE 4 8									
NE274									
NE145		T-							
NE125									
			-	-	-		•	**	
Z4	4 a	A	-CI	·G	- 	06-6	G	ጥር	Т
2.1		A							
GB358		A							
DK13		A							
GB809		A							
GBGGS	10	A	C	1		CG G	1	10	д
BE95	5 a	т-		۸	C_	CD		TC - A	m
DE 93	Ja			A	G	CA	ي	1CA	T
нк2	6-5		_mcc			m c	_	mc c	66m 6
nn2									
FR1	7.		C 177.0		7 00	_	_		
r K1	/a		-CTG	,C-A	A-GG	G	C	TG	GCT
VN4	0 -	m	~ m		_				
		T-		A	1	GW-G		TCG	GN
VN13	βD	- <u>A</u> - <u>A</u>	-1						
:D:10	0.	-				_			
VN12	Эa	A	-CTG	;T	~	C		TG	GCAA





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Fig.1J

HCV-1	1 a	500 TGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGG
HCV-J HC-G9 BNL1	1b 1c 1d	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
BNL2 FR2	ld 1f	N-ATCNGTNNNNNNNNNNNNN
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4 BNL5 BNL6	2b 2cd 2e 2f 2g 2h 2i	C
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	C
Z4 Z1 GE358 DK13 GE809 BNL7 BNL8 BNL9 BNL10 BNL11 BNL11	4 b	
BE95	5a	CACTGACTGGA
нк2	6a	CAGACAA-CGA-CT
FR1	7a	
VN4	8a	TNNCA-CGN-ATCN
VN12	9a	NATACCA-CGGA-A
NE9S	10a	AA-T <u>T</u> -TC





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Fig.1K

HCV-1	la	501 GAACCTTCCTG	GTTGCTCTT	тстста	TCTTCCTTCTGG	CCCTGCTCT	550 CTT
HCV-J	1b	TGC-			CT-A-	-TTG-	
HC-G9					T-GC-		
BNL1					CT		
BNL2					CT-A-		
FR2	II	KN-		-1414	CT	-NT-A	
HC-J6	2.5	T-ZC-		-т	T-G		-c-
HC-J8					TT-GT-		
S83	20	TT-GC-			TCT	CT-G-	
NE92	2d	T-GC-		-T	T-AT	A-	
BNL3					TNGT		
FR4					T-G		
BNL4					T-GT		
BNL5	2h	TGC-		-T	·T-G	TA-	
BNL6	21	G		T	T-A		
511110		C	Č	•			
NZL1	3a	T-GC-	c-	-T		-TT	
HCV-TR					-TCC-		
NE48					T-GT-		
NE274					T-GT-		
NE145	3e			-T	T-GT-	-TG-	- <u>A</u> -
NE125	3f	TT-GC-		-T	T-	-TCT	- <u>A</u> -
5 4					_		_
Z4					T		
Z1 GB358					TT-		
DK13					T-CT		
GB809					CT		
BNL7					CT		
BNL8					CT		
BNL9					·CT		
BNL10					·Y		
BNL11					·CT		
BNL12					A-C		
BNL12	47				M-C	-A1	-G-
BE95	5a	TT-AC-			ТАТ	-TT	-G-
HK2	6a	TCC-			T	-AA	-G-
FR1	7a	T	¢-	-T	CT- <u>A</u> -	-AA-	-G-
VN4					NCT		
VN12	9a	T			WCT		-G-
NE98	10a	TT-A				-TTT	-A-





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Fig.1L

	_
HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	551 1a GCTTGACTGTGCCCGCTTCGGCCTACCAAGTGCGCAACTCCACGGGGCTT 1b -TCA-CAGT-GGTTG-G 1cCA-CTGT-GGTTG-G 1dG-TAA-KA-CTCG-GG-AT-CG-A 1dG-TAA-A-CTC-TG-GG-AT-CG-A 1fC-CACA-CTTG-GA-G-A-AC-ATGGC
HC-J6 HC-J8 S83 NE92 ENL3 FR4 BNL4 BNL5 BNL6	2aA-CCACCG-TCCTGC-GAAGATGTACCGGC 2bG-CAA-TGTAGTGGCA-GATT-GTTCTAGC 2cA-CTA-TCGTGG-GCAAGGAGGC-ACTCC 2d -TA-CG-TCC-GTGGCAAGAGCA-CTC- 2e -TG-CCT-TCT-N-GTTG-GCAAATAGTCA-GCC 2f -TA-CCTG-TATAGTAAGAAGCCACT-C 2g -TG-CCT-TCTGTGGTAAGAGTACCA-G 2h -TC-CG-GCTGTGGCAAGAGCCACTC- 2iA-CCG-TCTGTGTGCGCGGTTTC-
NZI1 HCV-TR NE48 NE274 NE145 NE125	3a A-T-CATA-AG-CAGTCTAG-GTGG-TA-GT-TCC 3b TGCG-T-G-TAG-GTACACGA-GT-TCA 3c GTCTGTTAG-A-GGCT-G-GTACG-TGTAT-CCC 3d GTCTGTTG-A-GGATTGTACG-TGTGT-TCC 3e CT-TGCTAGTC-GG-TGG-G-TG-AT-CTC 3f GT-TCCAGGGCTAG-GTACA-GA-GT-CCA
Z4 Z1 GB358 DK13 GB809 BNL7 SNL8 BNL9 BNL10 BNL11 BNL12	4a C-CTAGTG-GCTACGTG-TTCA-C 4b CAACAAATGTGCTACGTG-TTCG-C 4c CTA-CGT-A-CTATTG-TTCA-C 4d CTGG-GTTA-CTATTG-TTCG 4e C
BE95	5a -TCCTGCTAGTT-CCTACATGT-TA
HK2	6aC-CAACATCTTACCTACGGTA
FR1	7aC-CACAACAAATTCAAGGT-TA-C
VN4	8aC-TAACAACCGGCGTTATACAAGT-TCG
VN12	9aC-CCACTCCACTAA-CTATGCTAAGT-TG
NE98	10aCT-ACAA-AG-C-GGCTGG-GTACTTGT-CAC





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Fig.1M

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	601 1a TACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTACGAGGCGGC 1bTGCCT-CAAA 1cTCCTT-CCCA-CTATA
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4	1fTTCTT-CGGCCCATAAA 2aATGGCCA-CTGATCACCGGCACTCCA 2bTCTTAACCCACCGGCCTCA 2cATGCCGCTCTCTGGCCTT-A 2dATGACAGAGTCCCGGCCTCAG 2eTATG-CACTCAACCCAGGC-ATTN 2fATG-CGTCTG-CTGACCCCGGCCTCAG 2gATG-CACTT-CAACCCACGGCAATCA
BNL5 BNL6	2hTATGGT-AAGCCC-GGCCTTAA 2iATGGT-GAGCCC-T-GGCCTC-A
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a GT-C-TCCTT-CTAGCTC-A 3b TGTGC-TCCTTGGC
24 21 GB358 DK13 GB809 BNL7 BNL8 BNL9 BNL10 BNL10 BNL11	4a -TA
BE95	5aTTT
нк2	6aA
FR1	7aTC-T
VN4	8aTC
VN12	9aTTC-ACTAGCCT <u>A</u> A
NE98	10aATGATCCAGGGTCTC-G





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Fig. 1N

HCV-1	651 700 la CGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCA
HCV-J	1b GCATGACCGCCGA-T-
HC-G9	1c GA-CCTGATCTGCTGC-AAC
BNL1	ldG-ATGATACAGCGAT-
BNL2	1d T-G-ATGTG-CATGCAA
FR2	lf GCATTGTNGCA-AGA
_	
HC-J6	2a G-CTGCGTCCGAGAAA-TG-
HC-J8	2b TCAG-TCTCTT-AAT-AGAATAATG
S83	2c A-GAAG-GTTTAT-AGACC-C
NE92	2d GTG-TTGTCCTT-AGGACA
BNL3	2e GCGG-GTTGTTATAGAA-AGCTC-C
FR4	2f GCGG-GCTGTTATCT-AGA-GTCAT-
BNL4	2g G-GCGG-GTTGTTATGT-AGTTGC
BNL5	2h GTG-GTGTCTATAT-AGA-GC-CCAA-
BNL6	2i GGGTGTCTATTCT-AGT-GAA
	The state of the s
NZL1	3a TTTACCTATC-AGC
HCV-TR	3b ATGTTTACAGCCACAACC
NE 48	3c -CTTTGCTACC-AAA-CAAT-
NE274	3d TA-TTTGA-T-T-G-CATCA
NE145	3e ATGTGTTCG-AGA-C
NE125	3f TATTGCCTGCACCT-
	10 0 0 1 0 0 140
24	4a -CCAATTGACTGATGACTG-
21	4b GC-CCAATTGATCTGGACAG-
GB358	4c GC-CCAACTCATT-ACGA-G-TTG-
DK13	4d TT-CCAT-ACTCATGA-GAG-
GB809	4e -ACAT-ACTCAACTGAAGACCG-
BNL7	4k -CCATCTCATGCGA-LG-
ENL8	4k -C-CCATCTATGCGA-DACTG-
BNL9	4k -CCATTCTCATGCGA-A-TG-
BNL10	4k -CCAT-AGCACTA-TGCGA-A-TG-
BNL11	4k -CCATCTAAGCGAAAA-
BNL12	41 -CCAT-ACTAATACTGAAGACTG-
	THE CI-GANGACIG-
BE95	5a TA-CCTGAG-ATTGTCATGACAT-
	_
HK2	6a T-C-ATGT-TTTGTAT-GT-GA-G-TC-ATG
ED 1	7 (1) (2) (2)
FR1	7a GACCATGATCTATTATA-CAAG-CG-
VN4	8a GACACTGTTTTGTT-AT-GAAGRT-RA
- · -	THE TENTH OF THE T
VN12	9a T-GCATGTCTCTCGAAGACC
NE98	10a GATTCTTATCTCACTCT





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Fig.10

	3	
	701	50
HCV-1	la ACGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGA	
HCV-J	1b -TTTCC-TCAC-CTCCGGA-	
HC-G9	1cCT-CC-T-GTCAG	
BNL1	1dCATCTCC-CCAC-CC-TGGTAAA-	
BNL2	ldT-T-TC-TCAC-RC-CC-TGGTAA	
FR2	lf -TATCC-TCACC-CCCAG-GCAT	
+ - \-	11 1M1 CC 1 C A AC-C-CCAG-GCAI	C
HC-J6	2a -TA-ATCCA-ACG-CT-AG-ATGTGCA-C-	_
HC-J8	2b G-AT-CATCA-ACAAG-AA-C-ACTGTG-AAC-	G
S83	25 G-H1-CA1CA-ACAAG-AHC-ACTGTG-AAC-	C
	2cTTC-A	A
NE92	2dATACC-CA-ACG-TT-GC-ATA-ATGTGCC-	Ą
BNL3	2e GTCGG-TCCACA-CCCT-GC-ACA-AGTGCA-	
FR4	2f -TAGGA-CTTCACAG-CT-GC-ACTGTGCCG	A.
BNL4	2g -TAAGCCCA-ACG-CTC-ACTGTG-ACC-	
BNL5	2h -TCAGTC-CCA-AC-TGAC-ATGTGCC-	
BNL6	2iACC-CCA-ACG-CACA-CTGTGCC-	<u> </u>
NZL1	3a -TA-AT-CCACCC-AGAAGTT-	C
HCV-TR	3b CAAATCACACAAG-CT-AA-GGTTAC	Č
NE48	3cAACCA-ACGTGAGGTTC-	
NE274	3dTCAACA-TCGG-AAAGGTT-A-T-	
NE145	3eA-AGACACCCGCAAAGTAT-	
NE125	3f CAGACAC-C-AG-AAGATGTAAC-	
24	4aA-AC-TCAC-CGGATGT-GCAC-	_
Z1	4b -TA-TTC-CCC-CTC-TG-GCCCT-	
GB358	4c -TCAGAC-CCCC-CTCCGG-GCCTT	
DK13	4dAAGT-CACT-TC-CCCTG-GCAAC	
GB809	4e CAG C CC-CTC-A GT-GCCTT-(
BNL7		_
	4k -TCAGAC-TCACC-TCCAG-GCCAT-(
BNT8	4k -TCAGAC-TCCC-TTCAG-GCCAT-(
BNL9	4k -TCAGTC	C
BNL10	4k CAGAC-CCCC-TCCAG-GCCAT-	C
BNL11	4k -TCATAC-CCCC-TCC-AG-GCCAT-	С
BNL12	41A-TC-CCCT-AACG-GCCCAT	A
BE95	5a -T-TGAGTACCCAATACT-AGCC-AGG	\square
HK2	6a -TCGGC-CCCATTGCCCTACCAA	_
FR1	7a -T-AGAC-AC-CC-TG-CTC-CT-AGT-CCCA-C	
		_
VN 4	8a -TCAACCCCA-GCCTGCCAGTGCC-A-C	_
		_
VN12	9aCTGA-C-ACTGCCTGATGGTGCA-A	_
NE98	10a -TA-AAACA-CC-TGGYCGTG-A-TCC	3
		_





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Fig.1P

		751 800
HCV-1	1a	GGCAAACTCCCCGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGG
HCV-J	1b	AGCAA-CACAA-ACGTCT
HC-G9	1c	TCGCGCGTC-GTGGGTGCTC-A
BNL1	1d	-CT-GTGA-TRGCAA-CGCTT
BNL2	1d	-CTTGTA-TGGCAA-CC-TGCTGT
FR2	1f	-CGCGCTATCGATGG-GGGCCCG
HC-J6	2a	CC-GGCGCT-ACA-GGCT-AGACGTCAGGAT
HC-J8	2b	CGGTGCG-T-A-TCGTAGCGACAGCA-A-T
S83	2c	CCTGGCGCT-T-A-T-A-GGCGGCAA-CA-CGAT
NE92	2d	CCTGGTGCG-TTA-C-A-GGCGGACGTTACCA-CA-T-C
BNL3	2e	CCTGGTGCT-T-A-C-A-GGAGGGCA-GTGCCG-CGAT
FR4	2£	CCTGGTGCT-T-A-T-GAGGTGGGCTACCA-CGAT
BNL4	2 σ	CC-GGCGC-T-A-T-G-GGCT-GGACGTCACCA-CGAT
BNL5	2h	CCTGGCGCG-T-A-C-G-GGTT-GGACGT-CACCA-CT-C
BNL6	21	CCTGGCGCG-TTA-C-A-GGCGGACATTCA-CAC
DNEO	2 -	CC166C6C6-11A-C-A-G6CGGACA11(A-CA1
NZL1	3.5	-T-GG-GCAA-TA-TG-TTC-A-ACATG-GCAT-AA
HCV-TR	3h	CTTGGCG-GAA-CGTC-A-CACCTG-GAAA
NE48	30	-T-GGTGCGAA-CG-ATC-A-CCG-GG-G
NE274	34	-CTGGCGCGAA-TG-ATC-A-CCATG-GGG
NE145	30	-CTGGTGCAA-GAG-TTCCG-ACG-AG-GTA
NE125	3 €	CCTGGCGCAGT-A-CG-ATCAA-CCA-GTG-GTA-G-G
NLIZO	JL	CCIGGCGCHGI-A-CG-AICAA-CCA-GTG-GT-A-GG
2.4	<i>A</i> =	CCGGGCGCTGCTTGA-TC-T-CGATG-GCT-AA-GA
Z1 Z1	1 d	CCCGCAGTTAGA-TCCA-GCA-GTG-ACA-GG
GB358	40	AT-GGCGCTGCTTGAATCCCGATG-GA-GA
DK13	4.4	MI GGCGCIGCTTGAATCC CATG-GA-GA
GB809	40	CTGTGCTGCTTGA-TCTT-GAG-GA-GG
	4.6	-T-GGTGCTGCTCGACCT-GGCTG-GCA-GA
BNL7	4 K	AT-GGCGCGACTTGA-TCTAGATG-GCTA-GG
BNL8	4 K	AT-GGCGCAGCTTGA-TCTGGATG-GA-GG
BNL9	4 K	AT-GGCGCAGCTTGA-TCCT-GGATG-GA-GG-
BNL10	4 K	AC-GCGGCGGCTTGA-TCCGGATG-GA-GG
BNL11	4 k	AT-GGCGCGACTTGA-TCTAGATG-GGA-GG
BNL12	41	CTTTCGGCTACTT-T-TCCG-AGGTG-GA-GG
	_	
BE95	5a	CT-GG-GCAGT-AG-T-CTGA-AGC-G-TCTACA-CG
	_	
HK2	6a	-CTTCCACGAGGAT-CCA-GTG-GTCG
		•
FR1	7a	TCATC-G-GAATCCACGG-TC-AG-ACCT
VN4	8a	-CGTCTACGA-TCCGG-T-CCAAATG-GCA-CA-GG
VN12	9a	-CGTCGG-GTATC-G-GGTG-CCGAGG-GCCT-GG
NE98	10a	CC-TGCGC-GA-CG-CTCTCCACGG-GA-A-GG





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Fig.1Q

HCV~1	l a	801 GAGCGCCACCCTCTGTTCGGCCCTCTACGTGGGGGACCTATGCGGGTCTG
HCV-J	1 b	-GCGTG-TCTA-GTTCAC-
HC-G9	10	-GCTG-GTTA-GT-ACCA
BNL1	1d	-G-NNGTCTA-GRT
BNL2	10	CAG-GT-TCCTA-GCAC-
FR2	1 €	-GCAGTGTCAA-GA-TTTGGC-
111/2	- -	
HC-J6	2 a	-TCGCCTTCTGGG-
HC-J8	2h	-GCATGGCCT-GTATG-GG-C-
s83	5.0	-TCTTGGTT-T
NE92	59	ATCTGT-TCTGA-AAGTCG-GC
BNL3	20	-TC
FR4	26	-TC
BNL4	2 -	-TC
	29	-GTTGTAA-CG-GTCG-G-
BNL5	2Ω 2.	$-\mathtt{TCT}-\mathtt{T}\mathtt{G}\mathtt{C}\mathtt{A}-\mathtt{TT}-\mathtt{G}-\mathtt{T}\mathtt{C}\mathtt{T}-\mathtt{C}\mathtt{CG}-\mathtt{A}-$
BNL6	23	-TCGICT-GT
NZL1	2.	
HCV-TR	2 h	CGCGGA-GCTGTTA-GTG
	ac	CGCACGACAAGGGGCT-TG
NE48	30	T-CG-T-AT-GA-TC-TTG-A-
NE274	30	AGCTTGT-GCCGGTTCTA-GTAG-C-
NE145	3e	C-TT-G-C-C-GTC-TTG-C-
NE125	3 T	TGCAG -G -GA -AT -T -AT T -GG
- A		
Z 4	4 a	CGCGTT-GTTTCAGG
Z1	4b	TGCGTTA-GCTA-TA-TA-TA
GB358	4 C	TGCTTGCGCCTTA-CAGTGGC-
DK13	4 d	CGTCCA-CAG-GTGG
GB809	4 e	TGCTG-GCCCCGTGGCT
BNL7	4 k	-GCTG-TA-CTT-RTYGGCT
BNL8	4 k	-GCTTG-TC-ATA-CTT-GTCGGCT
BNL9	4 k	-GCGTGATA-CTT-GTCGG
BNL10	4 k	AGCTTG-TATA-CYT-GTCGGCT
BNL11	4 k	-GCTTG-TAT-A-CT-GGCT
BNL12	41	TGCATA-CGTT-ACGG
BE95	5a	AG-G-TGC-C-GT-AAAGCG-TG-AC
HK2	6a	CGCAGTGG-TCATGA-CGTCC
FR1	7 a	-GCAGG-AT-TA-GA-CA-CA-CTTAGCA
VN 4	8a	CGCTG-GTATA-GTGGCC
		5555
VN12	9a	TGCTTG-GTCTA-GCTTGGGC
NE98	10a	RGCGACATAATAG-GC





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Fig.1R

	_
HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	851 1a TCTTTCTTGTCGGCCAACTGTTCACCTTCTCCCAGGCGCCACTGGACG 1b -TCTCGATCGT-TGA 1cCTGA-CTAC-CATGCATA 1dCC-CTG-ATAC-CTTGTCATA 1fCC-TGTAC-CTTGTCATA
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4 BNL5	2a -GA-GCA-CGATTGG-ACAATTT 2b -GA-GAC-ATCGGGCTTGG-AA-ACAAAACTTC 2c -GA-GG-CCTGG-CGGT-G-GG-ACAA-ATAC-TTT 2d -GA-GT-G-CTTCTG-CT-AGCAATTAA-TTT 2e -GA-GA-A-CT-CAGGCTT-G-GG-AG-AT-ACTTC 2f -GA-GA-A-CA-CGG-TGC-GT-GAGCAATATACTTTT 2g -GA-GA-A-CT-CTGG-TGTTGG-GCAA-ATAACTTT 2h -GA-GT-GTCTT-TTGACTCAAATCTTC
NZL1 HCV-TR NE48 NE274 NE145 NE125	3aC-G-AGCCGAGATC-ATCAA 3b -GG-AGCAGATC-CACC 3c -TCAAGCAAAGATC-CACA
Z4 Z1 GB358 DK13 GB809 BNL7 BNL8 BNL9 BNL10 BNL11	4a CCGA-GGGAATTCGGGC-T
BE95	5a -ACT-GAATAGGTC-C-AGGCT
HK2	6aT-G-CGATCAGC-C-TTT
FR1	7a -AA-CT-GAGGTTTAGGT-A-TATCA-GTT
VN4	Sa -TCCTAGCGCAGGTCATGTCA-GTT
VN12	9a
NE98	10a -A





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Fig.1S

		CTATCTATCCCGGCCATATAACGGGTCAC	
HC-G9 1		-CG-G <u>A</u>	
	-AG-AGC G-ACT	-A -CTCT-TC	
		-CCTTACCCTA	
		-CC-AATCCCC -CACGGCTA	-
		-CACACT <u>A</u> 1	
		-CACACAA	_
	-CG-AT TCG-AC	<u> </u>	
2 2144	1CG- X C	-GA	
		-GC-GCAC-TT-AA1	_
		-GACAG-TT-AA1 -AC-GCATG-TT-A1	-
		-AC-GCTTCT-AA	
		-GT-GCA	
		-CCA-T	
		-CCG-GGCG-TC	
		-CCA-AACAA	
	-CG-ACTT -TAT	-CCG-AGTC1	r
	-CG-AT	•	
	-CAC		
	-CG-AT		
	-CG-AAT FCACCT		
		-CTCAGTG-TCC	
		-CA-ACG-CCC	
FRI	-CG-ATC	NA-CN-TCG-C <u>A</u>	- <u>v</u> -
VN4 8	rcg-Agrcr	-CCA-AGCTA	
VN12 9	-CG-ACCT	-CG-ACCTG	
NE98 10	rcg-Accr-	·C	



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Fig.1T

	•	
HCV-1 HCV-J HC-G9 FR2	lb lc	951 957 CATGGCA T AT NNNNNNN
HC-J6 HC-J8 S83 NE92 BNL3 FR4	2b 2c 2d	G T GG G ANN
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	AT TT GTT
Z4 Z1 GB358 DK13 GB809	4b 4c 4d	GG GC GT GT
BE95	5a	G
нк2	6a	GT
FR1	7a	G
VN4	8a	<u>V</u>
VN12	9a	GG



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Fig.2A

HCV1 HCV-J	1ā 1b	1 MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRR-T
BNL1 BNL2 CAM1078	1d 1d	XXXXXXXXXXXXXX
FR2	le 1f	
HCJ6 HCJ8 CH610	2a 2b 2c	R-T
NE92	2c	R-T
BNL3	2e	R- <u>-</u>
FR4	2f	P-
HCVTR	3b	LRQTLV-
DK13	4d	R-TM
CAM600	4e	R-TM
GB809 BNL7	4e 4k	L-R-TM
DMT /	4 K	R-TM
BE95	5a	R-T <u>M</u>
HK2	6a	LR-TT
FR1	7a	LR-TM
VN4	8a	LR-TI
VN13	8b	LR-TI
VN12	9a	LR-TM
NE98	10a	LR-TXVV-



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Fig.2B

HCV1 HCV-J BNL1	1a 1b 1d	51 100 KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP
BNL2 CAM1078 FR2	ld le lf	B
HCJ6 HCJ8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	
HCVTR	3b	KQ-HLSRS
DK13 CAM600 GB809 BNL7	4d 4e 4e 4k	
BE95	5a	AL
HK2	6a	Q-QH
FR1	7a	V-Q-TS-G
VN4 VN13	8a 8b	V-HQT
VN12	9a	AV-QNQ
NE98	10a	SRTS



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Fig.2C

HCV1 HCV-J BNL1 BNL2 FR2	1a 1b 1d 1d 1f	101 150 RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARANNNS-T
HC-J6 HC-J8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	NHV
HCV-TR	3b	NF
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7	4 c 4 d 4 e 4 f 4 g 4 h 4 k	VV -XXNXVV NVV VV VV
BE95	5a	NKG-IV
HK2	6a	HNVVV
FR1	7a	NNVL-GVL-GV-A-
VN4 VN13	8a 8b	NNXXIE
VN12	9a	D-X-NXV-AE
NE 98	10a	N



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Fig.2D

HCV1 HCV-J	la lb	151 200 LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL
BNL1 BNL2 FR2	1d 1d 1d 1f	
	**	-XXGXXXXXXXXXTE-HST-DG
HC-J6 HC-J8	2a	I-T-VAE-K-ISTG
CH610	2ъ	
NE92	2c	
BNL3	2d	TV CT V maca
FR4	2 e	A
BNL4	2f	TTTTTTTT
BNL5	2g	
BNL5	2h	1
DIATO	2i	IIVVA-RS-S
HCV-TR	3b	A-GF
GB116	4c	-EAVISTVNYAS-V
DK13	4a	TNYAS-V
CAM600	4e	NYS-V
GB809	4e	AVIGVNYAS-V
G22	4 £	AVI
GB549	4 g	VHYH-TS-I
GB438	4h	AVI
BNL7	4 k	AVIVRQHYAS-I
BNL8	4 k	I-FINYVS-I
BNL9	4 k	I
BNL9	4 k	IINYH-TS-I
BNL10	4 k	IIXXTNYVS-I
BNL11	41	IXTNYVS-I
	_ _	IIQHYVS-I
BE95	5a	
HK2	ба	AII
FR1	7a	AIIK-AS-I
VN4	8a	XXIXX-X-X-X-XXTAHYT-KS
VN12	9a	
		-XAIIXTLNYA-KS
NE98	10a	I-FFLT-TAGLEYAS



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Fig.2E

HCV-1 HCV-J BNL1 BNL2 FR2	la lb ld ld lf	201 YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRDSIMDGM-M-YD-HLM-LL-VKXLSIMSGMAN-SMXLL-VK-
HC-J6 HC-J8 CH610 NE92 BNL3 FR4 BNL4	2a 2b 2c 2d 2e 2f 2g	S-GK-IXIIPLL-A-I -MT-DTWQLQA-VVEKVTIPVS-NVQQ -YAS-NTWQLTVLENDNGTLHIQVNVKH -MSWQLEG-VEQIPVS-NI-Q -MQWQLRVVEKKIIPVS-NI-VSQ -MAS-NWQLXVVENSSGRFHIPIS-NI-VSK -MA
BNL5 BNL6	2h 2i	-MAS-NIWQMQG-VVELQKIPVNVNQ -MSWQLKVVE-HQ-QIPVNVSQ -MSWQLEE-VVEWKD-TIPVNI-VSQ
HCVTR	3b	-VLS-GE-VLTTQ-STTVSTV-T
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7 BNL8 BNL9 BNL9 BNL9 BNL10 BNL11 GB724	40 40 40 41 41 41 41 41 41	I
BE95	5a	DNLAMTVQILSAPS
HK2	6a	LLDAMLLVDDR-TH-VL-IPN
FR1	7a	LS-NFETMLIKAELPVSL-VPN
VN12	8a	LETLLKXX-QQASL-VPN
NE98	9a 10a	LNGMLKTLTKLSASL-VQN -MS-GG-ILSTIPVSXVKS



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Fig.2F

		251 300
HCV-1	¹ 1a	GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT
HCV-J	1b	SSI-T-TIVA-AMSSYE-
BNL1	ld	ASV-TXAIVXX-FM-XAM-H-
BNL2	1d	ANV-TAAIVT-AFRMLYH-
FR2	1f	ANA-IDEVVA-VFM-IGTS
HC-J6	2a	PGALTQGTMV-MG-M-AA-M-IVOHF
HC-J8	2b	RGALTRST-V-MI-MAAVA-MILS-A-MVQNF
CH610	2c	PGTLTKGA-V-VI-MVALMIAA-AVIAQTF
NE 92	2d	PGALTKGTTIIAFIA-M-AS-V-IIOH-KF
BNI.3	2e	PGALTKGARAV-MVA-MIAA-A-IVA-KYF
FR4	2f	PGALTRGATI-MIA-MIAA-VAVVOY-TF
BNL4	2 a	PGALTRGTTI-MVIVA-MIAA-VVIVOH-NF
BNL5	29 2h	PGALTRG-TTI-AVF-A-M-S-F-MIOH-IF
BNL6	211 2i	PGAXTKGTIT-AF
BNTO	21	PGAXTRGT11-AF
HCVTR	3b	LGVTTASI-T-V-MARQAF-AART-
GB116	4 C	VGA-LESS-VMAVIGM-S-Q
DK13	4 c	LNA-LESQIVGQ
CAM600	4 e	AGA-LEPVMAMIGLMQ
GB809	4 e	VGA-LEPVMAVGLMQ
G22	4 f	LGA-LESMVMTGIAMRL
GB549	4 g	VGA-LESMVMAVIGMR
GB438	4ñ	LGA-L-SV-Q-VMAIHGAMVS-Q
BNL7	4 k	IGA-LESS-VMAVIX-XGLM-S-R
BNL8	4 k	IGA-LESS-VMAVIGLM-S-R
BNL9	4 k	IGA-LESS-VMAVIGAM-S-R
BNL9	4 k	TAA-LESS-VMAVI-XGLM-SXQ
BNL10	4 k	IGA-LESS-V-VMAVIGLM-S-R
BNL11	41	LSA-LMSVVMASGAMQ
GB724	4 x	VDA-LESFVMAVGAMO
	•••	
BE95	. 5a	LGAVTAPAV-Y-A-G-AAALMYRQ-A-
		·-
HK2	6a	ASTGFVA-A-VVSILAQ
FR1	7 a	SSV-IHGFVA-AFM-IIIR-KY-OV
		_
VN4	8a	AST-V-GF-K-V-IMA-AFMGLLRM-OV
VN12	9a	ASVSIRGV-E-VA-AFMGLRMYEI
NE 98	10a	PCAATAST-V-MM-XAALXG-SWRH-Q



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Fig.2G

HCV-1 HCV-J BNL1 BNL2 FR2	la lb ld ld lf	301 319 TQGCNCSIYPGHITGHRMA V-DVSE V-DSXXX
HC-J6 HC-J8 CH610 NE92 BNL3 FR4 BNL4 BNL5	2a 2b 2c 2d 2e 2f 2g 2h	V-DX V-DX V-DX V-D
HCVTR	3b	V-TV.S
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7 BNL8 BNL9 BNL9 BNL10 BNL11 GB724	4c 4d 4e 4f 4h 4k 4k 4k 4k	DAVDTDAVD
BE95	5a	V-NSV
нк2	6a	V-DTV
FR1	7a	DXNXV
VN4	8a	V-ET
VN12	9a	A-DA
NE98	10a	V-D



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Fig.3A

SEQ ID NO. 1 (BNL1, 1d)
ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCTCAKGGSGTN
NNNNNNCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGNNG

NNNNNCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGNNG GGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTCACAACCTCGTGGCAGGCGACAGCCTATCCCC AAGGCTCGYCGGYCCGAGGGCAGGTCCTGGGCTCAGCCCGGGTATCCTTGGCCCCTCTATGGCAAT GAGGGCTGCGGGTGGGCGGGNTGGCTCCTGTCCCCCCGCGGCTCTCGGCCCCAATTGGGGCCCC

SEQ ID NO. 3 (BNL1, 1d)

SEQ ID NO. 5 (BNL2, 1d)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGGACGTC
AAGNTCCCGGGTGGTCGAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGTTG
GGTGTGCGCGCGACCAGGAAGACTTCCGAGCGGTCGCAGCCTCGTGACAGGCGACAGCCTATTCCT
AAGGCTCGCCAGTCCGATGGCAGNNCCTGGGCTCAGCCAGGGCATCCCTGGCCCCTCTATGGCAAT
GAGGGCTGCGGATGGGCGGATGGCTCCTGTCCCCCCGCGGCTCTCGGCCCAGTTGGGGCCCC

SEQ ID NO. 7 (BNL2, 1d)

SEQ ID NO. 9 (CAM1078, le)



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Fig.3B

SEQ ID NO. 11 (FR2, 1f) ATGAGCACGAATCCTAAAACCTCAAAGAAAAACCAAACGCAACACCGACGCCCCACAGGACGTT AAATTCCCGGGTGGGGGCAGATCGTGGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGGTTG GGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGCGGAAGGC GACAGCCTATCCCCAAGGCTCGCCGACCCGAGGGCAGGTCCTGGGCTCAGCCTGGGTACC CATGGCCCCTCTATGCTAACGAGGGCTGCGGATGGCGGGATGGCTCCTGTCCCCTCGCG GCTCCCGTCCTAGCTGGGGCCCCAATGACCCCCGACGTAGATCACGCAATTTGGGTAAGG TCATCGATACCCTAACGTGTGGCTTCGCCGATCTCATGGGGTACATTCCGCTCGTCGGCGC CCCCCTAGGGGGCGCTTCCAGAACCCTGNCACATGGTGTCCGGGTCCTGGNAGGCGGCGTGATNNN NNNNNNNNAACCTTCCNGGTTGCTCTTTNNCTATCTTCCTCTTGGCNTTACTCTCTTGCCTCAC AGTCCCCACCTCTGCCTATGAGGTGCACAGCACAACCGATGGCTACCATGTCACTAATGACTGTTC CAACGGCAGCATCGTATATGAGGCAAAGGACATCATCCTTCACACGCCTGGGTGNGTGCCCTGCAT ${ t ACGGGAAGGCAATATCTCCCGTTGCTGGGTACCGCTCACCCCCACGCTCGCAGCGCGGATCGCGAA}$ CGCTCCCATCGATGAGGTGCGGCGTCACGTCGACCTCCTCGTGGGGGGCAGCCGTGTTCTGCTCAGC CATGTACATTGGGGACCTTTGTGGGGGGCGTCTTCCTCGTTGGGCAATTGTTCACCTTCACGTCCCG GCGGCATTGGACGGTGCAGGACTGTAATTGTTCCATTTACTCTGGCCACATAACGGGCCACCGNNN

SEQ ID NO. 13 (BNL3, 2e)
ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACCAACCGCCGCCCACAGGACGTC
AAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGATTG
GGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCAGCCACGTGGAAGGCGCCAGCCCATCCCT
AAAGATCGGNGNGCCACTGGCAGGTCCTGGGGACGTCCAGGATATCCCTGGCCCCTGTATGGGAAC
GAGGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCCGAGGCTCTC

SEQ ID NO. 17 (FR4, 2f) ATGAGCACAAATCCTAAACCTCAAAGAAAAACTAAAAGAAACACTAACCGTCGCCCACAGGAC GTTAAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAG GTTGGGTGTGCGCGCCCAAGGAAGACTTCTGAACGGTCCCAGCCACGTGGAAGGCGCCAGCCC ATCCCAAAAGATCGGCGCCCCCCTGGCAAGTCCTGGGGACGTCCAGGATACCCTTGGCCCCTGT ACGGGAACGAGGGCTCGGCTGGCCAGGGTGCTCCTCGCCCCCGGGGCTCTCGCCCCTCGTG GGGCCCAAACGACCCCGGCACAGGTCACGCAACTTGGGTAAGGTCATCGATACCCTCACGTG TGGCTTTGSCGACCTCATGGGGTACATACCTGTCGTCGGCGCCCCTGTGGGCGGCGTTGCCAGA GCCCTCGCGCATGGCGTGCGGGTCCTGGAGGACGGGATAAATTATGCAACAGGGAACTTGCCCGGT GTTAAGAACAACAGCCACTTCTACATGGCGACTAATGACTGTGCCAATGACAGCATCGTCTGGCAG CTCAGGGACGCGGTGCTCCATGTTCCTGGATGTGTCCCCTGTGAGAGGTCAGGTAATAGGACCTTC TGTTGGACAGCGGTCTCGCCCAACGTGGCTGTGAGCCGACCTGGTGCTCTCACTAGAGGTCTGCGG GCTCACATTGATACCATCGTGATGTCCGCCACCCTCTGCTCTGCCCTATACATAGGGGACCTATGC GGCGCTGTGATGATAGCAGCGCAAGTTGCCGTCGTCTCACCGCAATACCATACTTTTGTCCAGGAA TGCAACTGCTCCATATACCCAGGCCATATCACAGGACATCGAATGGNN



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Fig.3C

SEQ ID NO. 19 (BNL4, 2g)
GACGGGGTAAATTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCTTGTTGGCTCTT
CTGTCTTGTGTCACCGTGCCTGTCTCTGCCGTGCAGGTTAAGAACACCAGTACCATGTACATGGCA
ACCAATGACTGTTCCAACAACAGCATCATCTGGCAAATGCAGGGCGCGGTGCTTCATGTTCCTGGA
TGTGTCCCGTGTGAGTTGCAGGGCAATAAGTCCCGGTGCTGGATACCGGTCACCTCCCAACGTGGCT
GTGAACCAGCCCGGCGCCCTCACTAGGGGCTTGCGGACGCACATTGACACCATCGTGATGGTCGCT
ACGCTCTGTTCTGCACTCTACATCGGGGACGTGTGTGGCGCGGTGATGATAGCTGCTCAGGTTGTC
ATTGTCTCGCCGCAACATCACAACTTTTCCCAGGATTGCAATTGTTCCATC

SEQ ID NO. 21 (BNL5, 2h)
ATGAGCACAPATCCTARACCTCARAGARARACCARARGARACACTARCCGCCGCCCACAGGACGTT
AAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGGCCCCCGGTTG
GGTGTGCGCGCGACGAGGARACTTCCGAACGGTCCCAGCCACCGTGGGAGGCGCCAGCCCATCCCT
AAAGATCGGCGCTCCACTGGCAPATCCTGGGGACGTCCAGGATACCCTTGGCCCCTGTATGGGAAC
GAGGGCCTTGGTTGGGCAGGATGGCTCTTGTCCCCTCGAGGCTCTC

SEQ ID NO. 23 (BNL5, 2h)
GACGGGATAAACTACGCAACAGGGAATCTGCCCGGTTGCTCCTTTTCTATCTTCTTGCTGGCCTTG
CTATCCTGTCTCACTGTGCCGGCGTCCGCTGTGCAGGACACCAGCCACTCTTATATGGTG
ACCAATGATTGCTCAAACAGCAGCATTGTCTGGCAGCTTAAGGATGCTGTGCTTCACGTCCCTGGA
TGTGTTCCATGTGAGAGGCACCAAAATCAGTCTCGCTGCTGGATACCTGTGACACCCAATGTGGCC
GTGAGCCAACCTGGCGCGCTCACCAGGGGTTTGCGGACGCACATTGACACCATCGTTGCGTCTGCT
ACCGTCTGCTCAGCTTTGTATGTGGGCGACTTCTCGCGCGCAGTGATGTTGGTCTCCAATTTTTC
ATGATCTCCCCTCAGCACCACCATCTTCGTCCAGGATTGCAACTGCTCGATA

SEQ ID NO. 27 (BNL7, 4k)
ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCCCCATGGACGTT
AAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGGTTG
GGTGTGCGCGCGACTCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAGACGCCAACCTATCCCC
AAGGCGCGTCGATCCGAGGGAAGGTCCTGGGCACAGCCAGGATATCCATGGCCTCTTTACGGTAAT
GAGGGTTGCGGGTGGGCANNATGGCTCTTGTCCCCCCGCGGTTCTC

SEQ ID NO. 29 (BNL7, 4k)
GACGGGATCAATTTTGCAACAGGGAACCTCCCCGGTTGCTCCTTTTCTATCTTCTCTTTGGCACTC
CTCTCGTGCCTGACTGTCCCCGCTTCGGCCATCAACTATCGCAATGTCTCGGGCATTTACTATGTC
ACCAATGATTGCCCGAATTCAAGCATAGTGTATGAGGCCGACCATCACATCTTGCACCTCCCAGGT
TGCGTGCCCTGCGTGAGAGAGGGGGAATCAGTCACGTTGCTGGGTAGCCCTTACCCCTACCGTCGCA
GCGCCATACATCGGCGCCCACTTGAGTCTCTACGGAGTCATGTGGACTTGATGTGGGGGCCGCC
ACTGTTTGTTCAGCCCTTTACATCGGGGATTTTTTGTGGYGGCTTGTTCCTAGTCGGTCAGATGTTC
TCTTTCCGACCAAGGCGCCACTGGACTACTCAAGATTGCAATTGTTCCATC



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Fig.3D

SEQ ID NO. 35 (BNL10, 4k)
GACGGGATCAATTATGCAACAGGGAATATTCCCGGTTGCTCYTTTTCTATCTTCCTTYTGGCACTT
CTCTCGTGTCTGACTGTCCCCGCTTCGGCCACTAACTATCGCAACGTCTCGGGCATCTACCATGTC
ACCAATGACTGCCCGAATTCAAGCATAGTGTATGAGGCCGACCATCACATCTTAGCACTTCCAGGT
TGCGTGCCCTGCGTGAGAGTGGGGAACCAGTCACGCTGCTGGGTGGCCCTTACCCCTACCGTCGCA
GCGCCATACACCGCGGCGCCGCTTGAGTCCCTGCGGAGTCATGTGGATCTGATGTGGGAGCTGCC
ACTGTTTGTTCAGCCCTTTACATCGGGGAYTTGTGTGGCGGCTTGTTCTTGGTTGGTCAGATGTTC
TCTTTYCAGCCTCGGCGCCACTGGACTACCCAGGATTGCAATTGTTCCATC



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Fig.3E

SEQ ID NO. 43 (VN4, 7c) ATGAGCACACTTCCAAAACCCCAAAGAAAAACCAAAAGAAACACCATCCGCCGCCCACA GGACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGTGGAGTCTACTTGCTGCCGCGCAG GGGCCCGCGCTTGGGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCCAGCCCAGAGG TAGGCGCCAACCAATACCCAAAGTGCGCCACCAAACGGGCCGTACCTGGGCCCAGCCCGG CCGCGGCTCTCGCCCAAATTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAACTTGGG TAAAGTCATCGACACCCTTACTTGCGGCTTCGCCGACCTCATGGGGTATATCCCTGTCGTAG GCGCTCCGWTGGGAGGCGTCGCGGNGGCCTTGGCGCATGGGGTCANGGNCATCGAGGACGGNGTAA ATTACGCAACAGNGAATCTTCCCGGNNGCTCTNTCTCTATCTTNCTCTTGGCACTTCTCTCGTGCC TTACAACACCAGCCTCCGCGGCGCATTATACCAACAAGTCTGGCCTGTACCATCTCACCAACGACT GCCCCAACAGCAGCATCGTTTATGAGGCGGAGACACTGATTTTGCACTTGCCTGGGTGTGTACCTT GTGTGAAGRTGRACAATCAATCCCGGTGCTGGGTGCAGGCCTCCCCGACCCTGGCAGTGCCGAACG CAGCTATGTATGTGGGGGGACCTGTGCGGGGGGCCTTTTCCTCGTTGGACAGCTCTTCACGCTCAGGC CTCGGATGCATCAGGTTGTCCAGGAGTGTAACTGTTCCATCTACACAGGGCATATCACTGGACACC GAATGGCA

SEQ ID NO. 47 (VN12, 7d) ATGAGCACACTTCCAAAACCCCAAAGAAAACCAAAAGAAACACAAACCGTCGCCCAATGGATGTC AAGTTCCCGGGCGGCGGTCAGATCGTTGGTGGAGTCTACTTGTTACCGCGCAGGGGCCCACGTTTG AAGGTGCGCCAGAACCAAGGCCGAACCTGGGCTCAGCCTGGGTACCCCTGGCCCCTTTATGGGAAC GAGGGCTGCGGCTGGCCGGGCTCTTGTCCCCCCGTGGCTCTCGCCCGGACTGGGGNCCCAAT GACCCCCGGNGGAGGTCCCGCAACCTGGGTAAGGTCATCG ACACCCTCACTTGCGGCTTCGCCGACCTCATGGAGTACATCCCTGTCGTTGGCGCCCCCCT TGGAGGCGTTGCGGCGGAACTGGNACATGGTGTCAGGGCCATCGAGGACGGGATAAACTATGCAAC AGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCWCTTGGCACTTCTCTCGTGCCTCACCACGCC TGCCTCCGCACTAAACTATGCTAACAAGTCTGGGCTGTATCATCTAACCAATGACTGCCCCAATAG CAGCATTGTGTATGAGGCGAATGGCATGATCCTGCATCTCCCGGGTTGCGTCCCCTGCGTGAAGAC CGGCAACCTGACCAAGTGTTGGCTGTCGGCCTCCCCGACATTGGCGGTGCAGAATGCGTCGGTGTC CGTGGGCGACTTATGCGGTGGGCTCTTTCTCGTTGGGCAGTTGTTCACGTTCAGACCCAGGATGTA TGAGATCGCCCAGGACTGCAACTGTTCCATCTATGCAGGCCACATCACTGGGCACCGGATGGCG

SEQ ID NO. 41 (FR1, 9a) ATGAGCACACTTCCAAAACCCCAAAGAAAACCAAAAGAAATACTAACCGTCGCCCTATGGAC GTCAAGTTCCCGGGCGGCGGCCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGC CCTCGTTTGGGTGTGCGCGCGACGAGAAAGACCTCCGAACGGTCCCAGCCTAGAGGCAGG CGCCAGCCCATACCAAAGGTACGCCAGCCGACAGGCCGTAGCTGGGGTCAACCCGGCTAC CCTTGGCCCCTTTATGGCAACGAGGGCTGCGGATGGGCGGGATGGCTCCTGTCCCCCGC GGGTCTCGTCCTAATTGGGGCCCCAACGACCCCCGGCGAAGGTCCCGCAACTTGGGTAAG GTCATCGATACCCTTACATNCGGNCTAGCCGACCTCATGGGGTACATCCCTGTCCTAGGAGG GCCGCTTGGCGGCTTGCCGCTGGCGCATGGCGTTAGGGCAATCGAGGACGGGGTCAATTA CGCAACAGGGAATCTTCCTGGTTGCTCCTTTTCTATCTTCCTCTTAGCACTGTTATCGTGCCTCAC TACACCAGCCTCAGCAATTCAAGTCAAGAACGCCTCTGGGATCTACCATCTTACCAATGACTGCTC GAACAACAGCATCGTTTTTGAGGCGGAGACCATGATACTGCATCTTCCAGGTTGTGTCCCATGTAT CAAGGCGGGGAATGAGTCACGATGTTGGCTCCCTGTCTCCCCCACCTTAGCCGTCCCCAACTCATC AGTGCCAATCCACGGGTTTCGCCGACACGTAGACCTCCTCGTTGGGGCAGCGGCATTTTGTTCGGC CATGTACATCGGAGACCTCTGTGGTAGCATAATCTTGGTAGGGCAGCTTTTTACTTTCAGGCCTAA GTACCATCAGGTTACCCAGGATTGTAACTGCTCTATNAACNCTGGCCACGTCACGGGACACAGGAT GGCA



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Fig.3F

SEQ ID NO. 49 (NE98, 10a)

ATGAGCACACTTCCTAAACCACAAAGAAAAACCAAAAGAAACACCAACC?CCGGCCACAGGACGTT
AAGTTCCCAGGCGGCGGTCAGATCGTTGGTGGAGTTTACGTGCTACCACGCAGGGGCCCCCAGTTG
GGTGTGCGTGCAGTGCGCAAACCTTCCGAGCGGTCCCCCAACCCATCCCC
AGGGCGCCCGAACCGAGGCAGGTCCTGGGCTCAGCCCGGGTACCCTTTGGCCCCTATATGGGAAT
GAGGGCTGCGGGTGGGCAGGGTGCCTCTGTCCCCGCGCGCTCTC

SEQ ID NO. 51 (NE98, 10a)

SEQ ID NO. 53 (BNL1,1d)

SEQ ID NO. 55 (BNL2,1d)

CTCGACAGTTACTGAGAACGACATCCGTACCGAGGRATCAATCTATCAATGTTGTGACTTGGCCCC
YGAGGCCCGCAAGGCCATAAAGTCGCTCACCGAGCGGCTGTACGTCGGGGGCCCCCTAACCAATTC
AAAGGGGCAGAACTGCGGCTATCGTCGGTGTCGCGCTAGCGGCGTGCTGACCACCAGCTGCGGCAA
CACCCTCACATGCTACTTGAAAGCCAGGGCGGCCTGTCGAGCTGCAAAGCTCCAGGACTGCACGAT
GCTCGTGTGCGGAGACGACCTTGTCGTTATCTGTGAGAGCGCGGGAGTCGAGGAGGACGCGGGGAA
CCTACGAGTC

SEQ ID NO. 57 (FR17,1d)

SEQ ID NO. 59 (CAM1078, 1e)

CGTACAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAG
TACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGA
GATTTGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTG
TGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCAT
GAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCCACAGGA
CGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGCTCTACCGCGCAGCGG
CCCTAGATTGGGTGTGCGCGCAGCGCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAG
GCGCCAACCTATTCCCAAGGAGCGCCGACCCGAGGTCCTGGGCGCAGCCCGGGTA
CCCCTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCCAGGTCCTGTCCCCTCG
CGGCTCCCGTCCTAGTTGGGGTCCTACTGACCCCCGGCGTAGGTCACCCAATTTGGGTAA
GGTCATCGATACCCTCACGTGTTGNTTCGCCGACCTCATGGGGTACATACCG



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Fig.3G

SEQ ID NO. 61 (CAM1078, le)

CTCAACGGTCACTGAAGCTGATATCCGAACAGAGGAGTCCATATACCAATGCTGTGACCTGCACCC
CGAAGCACGTGTAGCCATCAAGTCTTTGACTGAAAGGCTGTACGTCGGGGGGCCCTTGACCAATTC
AAAAGGGGAGAACTGCGGCTATCGCAGATGCCGTGCCAGCGGCGTCTTGACAACCAGCTGCGGCAA
CACCCTCACCTGCTATATCAAGGCCCTAGCAGCCTGTAGAGCTGCCAAGCTCCAGGACTGCACCAT
GCTCGTCTGTGGCGACGACCTGGTCGTGATCTGCGAGAGTGTAGGGACCCAGGAGGATGCGGCGAG
CCTGCGAGCC

SEQ ID NO. 63 (FR2, 1f)

NTCAACAGTCACTGAGAGTGATATCCGTACAGAGGAGTCCATCTACCAATGCTGTGATCTAGACCC CGAGGCTCGCAAGGCCATAAGGTCCCTCACAGAGAGGCTTTATATCGGGGGTCCCCTGACAAACTC AAAAGGGCAGAACTGCGGCTACCGCCGATGCCGTGCAAGCGGCGTCCTGACGACTAGCTGCGGCAA CACCCTCACCTGTTACATAAAGGCCAGGGCAGCCTGTCGAGCTGCGAAGCTCCAGGATTGCTCAAT GCTCGTCTGTGGCGACGACCTTGTCGTTATCTGCGAGATCGAGGGGTCCANGAGGATCCGTCGAN NNNNNNNNN

SEQ ID NO. 65 (FR16,1g)

CGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACATC
AACCGCCGCCCACAGGACGTCAAGTTCCCGGGCGGTGGCCAGATCGTCGGTGGAGTTTAC
CTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGG
TCGCAACCTCGTGGGAGGCGACAGCCTATCCCCAAGGCTCGCCGATCCGAGGGCAGGTCC
TGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGTTGGGCAGGG
TGGCTCCTGTCCCCCCATGGCTCCCGGCCTAGTTGGGGCCCTTCAGACCCCCGGCGTAGG
TCGCGTAATTTGGGTAAGGTCATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGG
TACATTCCGCTCGTCGGCGCCCCCCTAGGGGGCGTTGCCAGGGCCCTGGCGCAAGGCTTC
CGGGATCTACCACGTCACCAACGATTGTTCCAATGGGAACCATTGTGTATGAGGCGGAAGG
CATGATCATGCATCTCCCCGGGTGCCTCGCGTTCGGGAAGGTAATATCTCTCGTTG
CTGGGTACCGTTTTCCCCCACGCTCGCAGCCAGGAATGCTAGCGTCCCCACTCAGGCAAT
TCGGCGACACGTCGACTTGCTTGTTGGGGCCGCCACCTCTGTTCTCCTCACAWCCCGCCAGNA
CTACACAGTGCAAGACTGCAATTGTTCCATCTACCCCGGCCATATAACGGG

SEQ ID NO. 67 (FR16,1q)

SEQ ID NO. 69 (BNL3, 2e)

CTCGACAGTCACAGAGAGAGATATAAGNACTGAGGAGTCCATATACCAGGCTTGTTCCTTACCCGA GCAGGCCAGAACTGCCATACACTCATTGACTGAGAGACTCTACGTAGGAGGGCCCATGATGAACAG CAAAGGGCAATCCTGCGGATACAGGCATTGCCGCGCCAGCGGAGTGCTCACCACCAGTATGGGGAA TACCATCACGTGCTACATCAAGGCCCTAGCGGCTTGTAAAGCAGCAGGAATAGTGGCCCCCACCAT GCTGGTGTGCGGCGATGACCTAGTTGTCATCTCAGAGAGTCAGGGAGTCGAGGAGGACGACCGGAA CCTGANNNNN



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Fig.3H

SEQ ID NO. 71 (FR4, 2f)

CTCAACCGTCACAGAGAGGGATATAAGAACTGAGGAGTCCATATACCTGGCCTGCTCCTTACCCGA GCAGGCCCGGACTGCCATACATTCATTAACTGAGAGACTTTACGTGGGAGGGCCCATGATGAACAG CAAAGGGCAGTCCTGCGGATACAGGCGTTGCCGCGCTAGCGGAGTGCTCACCACCAGTATGGGGAA CACCATCACGTGTTATGTGAAAGCCCTCGCAGCTTGTAAAGCTGCGGGCCATTGTTGCCCCCACGAT GCTGGTGTGCGGCGATGACCTGGTTGTCATCTCAGAGAGTCAGGGGGCTGAGGAGGACGAGCGAAA CCTGAGAGTC

SEQ ID NO. 73 (BNL5,2h)

CTCAACAGTCGCGGAGAGAGACATCAGGACCGAGGAGTCCATTTACCTTGCCTGCTCCTTACCCGA GCAAGCCCGAACTGCCATACATTCATTGACTGAGAGACTTTACGTAGGAGGGCCCATGATGAACAG CAAGGGACAGTCCTGCGGTTACAGACGTTGCCGCGCCAGCGGAGTGCTCACCACCAGCATGGGGAA TACCATCACATGCTATGTGAAGGCATTAGCTGCCTGCAAAGCTGCAGGCATCGTTGCTCCCACGAT GCTGGTTTGTGGCGACGATCTGGTCATCATCTCAGAGAGTCAGGGAACCGAGGAGGATGAGCGGAA CCTGAGAGTC

SEQ ID NO. 75 (FR13, 2k)

CGNACANCCTCCAGGCCCCCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAG TACACCGGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATAAACCCACTCTATGCCCGGC CATTTGGGCGTGCCCCGCAAGACTGCTARCCGAGTAGCGTTGGGTTGCGAAAGGCCTTG TGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCATCAT GAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACTAACCGCCGCCCACAGGA CGTTAAGTTCCCGGCGGTGGCCAGATCGTTGGCGGAGTATACTTGTTGCCNTGCAGGGG NCCCAGGTNGNGTNTATGCGCAACGANGAAGACTNCCGAACAGTCCCAGCCACGTGGGAG GCGCCAGCCCATCCCGAAAGATCGGNGCACCACTGGCAAGTCCTGGGGACGTCCAGGATA TCCCTGGCCCCTGTATGGGAACGAGGGCCTCGGGTGGGCAGGGTGGCTCCTGTCCCCCCG GGGCTCCCGCCGTCATGGGGCCCCACGGACCCCCGGCATAGGTCGCGCAACTTGGGTAA GGTCATCGATACCCTCACGTNCGGCTTTNCCGACCTCATGGGGTACATTCCCGTCGTTGG CGCCCCAGTAGGNGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGG TCTGTCCTGAATTACCGNGCCAGTTTCTGCTGTGGAAATCAAAAACACCAGMAACACATA CATGGTGACTAACGACTGTTCAAACAGYAGCATCACCTGGCAGCTTNNGNNCGCGGTGCT TCACGTTCCTGGATGCGTCCCCTGTGAACGAGGGCCAACAGTTCCCGGTGCTGGATTCC AGTCACGCCCRACGTAKNCGTGAGCCGACCTGGTGCCCTAACCGAGGGTTTGCGATCGCA CATCGACACCATCGTAGCGTCCGCAACATTTTGTTCTGCCCTCTACATAGGGGATGTATG TGGCGCGATAATGATAGCTGCCCAAGTGGTCATCGTCTCGCCGGAGCATCATCACTTTGT CCAGGACTGTAACTGTTCCATCTACCCGGGCCACATAACGGGGCCTCGTATGTNG

SEQ ID NO. 77 (FR13, 2k)

ATCCACAGTCACTGAAAGAGACATCAGAGTTGAAGAGTCCGTTTATCTGTCCTGTTCACTTCCCGA GGAGGCCCGAGCTGCCATACACTCACTAACTGAGAGGCTGTACGTGGGAGGTCCCATGCAGAACAG CAAGGGGCAATCCTGCGGATACAGGCGCTGCCGCGCCAGCGGGGTGCTCACCACTAGCATGGGGAA TACTCTCACATGCTACTTGAAGGCCCAGGCGGCCTGCAGGGCCGGGGCATTGTTGCACCCACAAT GCTGGTGTGTGGCGACGACCTGGTCGTCATCTCAGAGAGTCAGGGGACTGAGAGGACGAGAACAA CCTGAGACCT



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Fig.3I

SEQ ID NO. 79 (FR18,21)

CTCAACAGTCACGGAGAGGGACATCAGGAATGAGGAGTCCATATTCCTGGCCTGCTCGTTGCCCGA GGAGGCCCGGACTGTCATACATTCGCTCACTGAGAGACTCTACATAGGCGGGCCGATGATGAACAG CAAAGGCCAGTCCTGTGGATACAGGCGTTGTCGCGCCAGCGGGGTGTTCACCACTAGCATGGGCAA TACCATCACGTGCTATGTGAAAGCCATGGCAGCTTGCAGAGCTGCCGGGATTGACGCCCCCACAAT GTTGGTATGTGGCGACGACCTGGTGGTCATCTCAGAGAGTCAGGGGACCGAGGAGGACGAAA TCTGAGAGTC

SEO ID NO. 81 (PAK64,3q)

CTCTTGACTCTACTGTCACTGAACAGGATATCAGGGTAGAAGAAGAAATATACCAATGTTGTGACC
TTGAGCCGGAGGCTAGACGGGCAATCAAATCGCTCACGGAACGGCTTTACGTTGGAGGTCCCATGT
TCAACAGCAAGGGGCTCAAATGCGGATATCGCCGTTGCCGTGCTAGCGGTGTATTGCCCACTAGCT
ACGGTAATACAATCACCTGCTACATCAAGGCCAGAGCGGCTGCTCGAGCTGCGGGCCTTCAAGACC
CATCATTCCTTGTCTGCGGAGATGATTTGGTGGTAGTGGCTGAGAGTTGCGKCGTTGATGAGGAGG
ATAGGGCAGC

SEQ ID NO. 83 (BNL8,4k)

SEQ ID NO. 85 (BNL12,41)

CTCCACGGTGACTGAAAAGGACATCAGGGTCGAGGAAGAGATCTATCAATGTTGTGACCTGGARCC CGAAGCCCGCAAAGCAATATCCGCCCTCACAGAGAGAGACTCTACTTGGGCGGCCCCATGTATAACAG CAAAGGGGAGCTCTGCGGGTATCGGAGGTGCCGCGAGCGGAGTGTACACCACAAGTTTCGGGAA CACAGTGACCTGCTATCTTAAGGCCACCGCAGCTACCAGGGCTGCAGGCCTAAAAGACTGCACCAT GCTGGTCTGCGGTGACGACTTCGCCGAGAGCGAGGGCGTAGAGGAGGATTCCCAACC CCTCCGAGCC

SEQ ID NO. 87 (EG61, 4m)

SEQ ID NO. 89 (VN13,7a)

CTCAACAGTCACAGAGCGCGATGTCCAGACGGAGCATGACATCTACCAGTGCTGTAAGTTGGAGCC CGCAGCACGGACAGCCATCACATCGCTTACTGACCGATTGTACTNCGGTGGTCCCATGTNTAACTC TAAAGGTCAGGCATGTGGATACCGTAGGTGCAGGGCCAGTGGCGTCTTGACCACCATCCTGGCCAA TACTCTGACTTGCTACTTGAAAGCTCAGGCGGCATGCAGAGCTGCCGGGCTGAAGGACTTTGACAT GTTGGTCTGCGGAGACGACCTTGTCGTTATTTCGGAGAGTTTGGGGGTCTCGGAGGACACTAGTGC ACTGCGAGCT



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Fig.3J

SEQ ID NO. 91 (VN4,7c)

SEQ ID NO. 93 (VN12,7d)

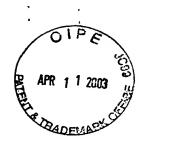
SEQ ID NO. 95 (FR1, 9a)

SEQ ID NO. 97 (NE98, 10a)

SEQ ID NO. 99 (FR14,11a)

SEQ ID NO. 101 (FR15, 11a)





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Fig.3K

SEO ID NO. 103 (FR19,11a)

CGTACAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACC
GGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATTAACCCACTCTATGCCCGGAGATTTGGGCGTG
CCCCCGCAAGACTGCTAGCCGAGTAGCGTTGGGTTGCGAAAGGCCTTGTGGTACTGCCTGATAGGG
TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAG
ACAAACCAAAAGAAACACCAACCGCCGCCCACAGGACGTTAAGTTCCCGGGCGGTGGCCAGATCGT
TGGCGGGGTGTACTTGTTGCCGCGCAGGGGCCCCAACCTATCCCCAAGGTTAGGCGCACCACCGGCCGTT

SEQ ID NO. 105 (FR19,11a)

CTCTACTGTCACAGAGAGGGATATACGAACAGAGGAATCCATYTATCTGGCTTGTCAATTGCCCGA AGAGGCCCGGAAGGCCATCAAATCACTGACAGAGAGACTATACGTGGGCGGCCCGATGGAAAACAG CAAGGGCCAGGCCTGCGGATACAGGCGTTGCCGCGCAAGCGGGGTATTCACCACAAGCTTGGGGAA CACCATGACTTGTTACATCAAAGCCAAGGCGGCTTGTAAAGCCGCTGGCATTGTTGACCCAGTGAT GCTCGTGTGCGGCGACGACCTAGTGGTCATCTCAGAAAGCAAGGGGGTGGAGGAGGACCAACGAGA CCTACGANTC

SEQ ID NC. 2 (BNL1, 1d)

MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRGRRQPIP KAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP

SEQ ID NO. 4 (BNL1, 1d)

DGVNYATGNLPGCSFSIFLLALLSCLTVPXTAHEVRNASGVYHVTNDCSNSSIIYEMDGMIMHYPGCVPCVREDNHLRCWMALTPTLAVKXASVPTXAIRRHVDLLVGXXTFCSAMYVXDLCGSVFLAGQLFTFSPRMHHTTQECNCSI

SEQ ID NO. 6 (BNL2, 1d)

MSTNPKPQRKTKRNTNRRPQDVKXPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRDRRQPIP KARQSDGXXWAQPGHPWPLYGNEGCGWAGWLLSPRGSRPSWGP

SEQ ID NO. 8 (BNL2, 1d)

DGVNYATGNLPGCSFSIFLLAFLSCLTVPTTAHEVRNASGVYHLTNDCSNSSIIYEMSGMILHAPG CVPCVRENNSSRCWMXLTPTLAVKDANVPTAAIRRHVDLLVGTAAFRSAMYVGDLCGSVFLVGQLF TFSPRLYHTTOECNCSI

SEQ ID NO. 10 (CAM1078, le)

MSTNPKPORKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP KERRPEGR

SEQ ID NO. 12 (FR2, 1f)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KARRPEGRSWAQPGYPWPLYANEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKVIDTLTCGFAD LMGYIPLVGAPLGGASRTLXHGVRVLXGGVXXXXXNLXGCSXXIFLLXLLSCLTVPTSAYEVHSTT DGYHVTNDCSNGSIVYEAKDIILHTPGXVPCIREGNISRCWVPLTPTLAARIANAPIDEVRRHVDL LVGAAVFCSAMYIGDLCGGVFLVGQLFTFTSRRHWT VODCNCSIYSGHITGHXXX

SEQ ID NO. 14 (BNL3, 2e)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KDRXATGRSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWG

SEQ ID NO. 16 (BNL3, 2e)

TCXXADLMGYXPVVGAPVGGXARALAXGVRVLEDGINYXTGNLPGCSFSIFXLALLSCVTVPVSXV EVKNTSQAYMATNDCSNNSIVWQLXDAVLHVPGCVPCENSSGRFHCWIPISPNIAVSKPGALTKGL RARIDAVVMSATLCSALYVGDVCGAVMIAAOAFIVAPKRHYFVOECNCSIYPGHITGHRMA





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Fig.3L

SEQ ID NO. 18 (FR4, 2f)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRAPRKTSERSQPRGRRQPIP
KDRRATGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNLGKVIDTLTCGFXD
LMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLSCITVPVSAIQVKNNS
HFYMATNDCANDSIVWQLRDAVLHVPGCVPCERSGNRTFCWTAVSPNVAVSRPGALTRGLRAHIDT
IVMSATLCSALYIGDLCGAVMTAAQVAVVSPQYHTFVQECNCSIYPGHITGHRMX

SEQ ID NO. 20 (BNL4, 2g)
DGVNYATGNLPGCSFSIFLLALLSCVTVPVSAVQVKNTSTMYMATNDCSNNSIIWQMQGAVLHVPG
CVPCELQGNKSRCWIPVTPNVAVNQPGALTRGLRTHIDTIVMVATLCSALYIGDVCGAVMIAAQVV
IVSPQHHNFSQDCNCSI

SEQ ID NO. 22 (BNL5, 2h)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGRSLAEYTCARRGKLRRSSMG

SEQ ID NC. 24 (BNL5, 2h)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAVQVKNTSHSYMVTNDCSNSSIVWQLKDAVLHVPG
CVPCERHQNQSRCWIPVTPNVAVSQPGALTRGLRTHIDTIVASATVCSALYVGDFCGAVMLVSQFF
MISPOHHIFVODCNCSI

SEQ ID NO. 26 (BNL6, 2i)
DGINYATGNLPGCSFSIFLLALLSCITVPVSAVQVANRSGSYMVTNDCSNSSIVWQLEEAVLHVPG
CVPCEWKDNTSRCWIPVTPNIAVSQPGAXTKGLRTHIDIIVASATFCSALYV

SEQ ID NO. 28 (BNL7, 4k)
MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
KARRSEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPSWGPNDPRRRSR

SEQ ID NO. 30 (BNL7, 4k)
DGINFATGNLPGCSFSIFLLALLSCLTVPASAINYRNVSGIYYVTNDCPNSSIVYEADHHILHLPG
CVPCVREGNQSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDXCXGLFLVGQMF
SFRPRRHWTTQDCNCSI

SEQ ID NO. 32 (BNL8, 4k)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAINYRNTSGIYHVTNDCPNSSIVYEADHHILHLPG
CVPCVRTGNQSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDLCGGLFLVGQNF
SFRPRRHWTAQDCNCSI

SEQ ID NO. 34 (BNL9, 4k)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAINYHNTSGIYHITNDCPNSSIVYEADHHILHLPG
CVPCVRVGNQSSCWVALTPTIAAPYIGAPLESIRSHVDLMVGAATVCSALYIGDLCGGAFLVGQMF
SFRPRRHWTTQDCNCSI

SEQ ID NO. 36 (BNL10, 4k)
DGINYATGNIPGCXFSIFLXALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVYEADHHILALPG
CVPCVRVGNQSRCWVALTPTVAAPYTAAPLESLRSHVDLMVGAATVCSALYIGXLCGGLFLVGQMF
SXQPRRHWTTQDCNCSI

SEQ ID NO. 38 (BNL11, 4k)
DGINYATGXLPGCSFSIFLLALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVFEADHHILHLPG
CVPCVKEGNHSRCWVALTPTVAAPYIGAPLESLRSHVDVMVGAATVCSALYIGDLCGGLFLVGQMF
SFRPRHWTTQECNCSI

SEQ ID NO. 40 (BNL12, 41)
DGINYATGNLPGCSFSIFILALLSCLTVPASAQHYRNVSGIYHVTNDCPNSSIVYESDHHILHLPG
CVPCVKTGNTSRCWVALTPTVAAPILSAPLMSVRRHVDLMVGAATLSSALYVGDLCGGAFLVGQMF
TFQPRRHWTVQDCNCSI



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Fig.3M

SEQ ID NO. 46 (VN13, 7a)

MSTLPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPXGSRPNWGPNDPRXRSRNLGKVIDTLTXXFADLIEYI

SEC ID NO. 44 (VN4, 7c)

MSTLPKPQRKTKRNTIRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRSRNLGKVIDTLTCGFAD LMGYIPVVGAPXGGVAXALAHGVXXIEDXVNYATXNLPXXSXSIXLLALLSCLTTPASAAHYTNKS GLYHLTNDCPNSSIVYEAETLILHLPGCVPCVKXXNQSRCWVQASPTLAVPNASTPVTGFRKHVDI MVGAAAFCSAMYVGDLCGGLFLVGQLFTLRPRMHQVVQECNCSIYTGHITGHRMA

SEQ ID NO. 48 (VN12, 7d)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQARGRRQPIP KVRQNQGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPDWXPNDPRXRSRNLGKVIDTLTCGFAD LMEYIPVVGAPLGGVAAELXHGVRAIEDGINYATGNLPGCSFSIFXLALLSCLTTPASALNYANKS GLYHLTNDCPNSSIVYEANGMILHLPGCVPCVKTGNLTKCWLSASPTLAVQNASVSIRGVREHVDL LVGAAAFCSAMYVGDLCGGLFLVGQLFTFRPRMYEIAQDCNCSIYAGHITGHRMA

SEQ ID NO. 42 (FR1, 9a)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKVRQPTGRSWGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLGKVIDTLTXXLADLMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLALLSCLTTPASAIQVKNASGIYHLTNDCSNNSIVFEAETMILHLPGCVPCIKAGNESRCWLPVSPTLAVPNSSVPIHGFRRHVDLLVGAAAFCSAMYIGDLCGSIILVGQLFTFRPKYHQVTQDCNCSXNXGHVTGHRMA

SEQ ID NO. 50 (NE98, 10a)

MSTLPKPQRKTKRNTNXRPQDVKFPGGGQIVGGVYVLPRRGPQLGVRAVRKTSERSQPRSRRQPIPRARRTEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRR

SEQ ID NO. 52 (NE98, 10a)

DGINFATGNLPGCSFSIFLLALFSCLLTPTAGLEYRNASGLYMVTNDCSNGSIVYEAGDIILHLPGCVPCVRSGNTSRCWIPVSXTVAVKSPCAATASLRTHVDMMVXAATLCSALYVGDLCGALFLXGQGFSWRHRQHWTVQDCNCSI

SEQ ID NO. 54 (BNL1,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERLYIGGXLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLRDCTMLVCGDDLVVICESAGVEEDAANLRA

SEQ ID NO. 56 (BNL2, 1d)

STVTENDIRTEXSIYQCCDLAXEARKAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLQDCTMLVCGDDLVVICESAGVEEDAANLRV

SEQ ID NO. 58 (FR17,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLQDCTMLVCGDDLVVICESMGVEEDAANLRV



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Fig.3N

SEQ ID NO. 60 (CAM1078, le)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP KERRPEGRSWAQPGYPWPLYGNEGCGWAGXLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCXFAD LMGYIP

SEQ ID NO. 62 (CAM1078, 1e)

STVTEADIRTEESIYQCCDLHPEARVAIKSLTERLYVGGPLTNSKGENCGYRRCRASGVLTTSCGN TLTCYIKALAACRAAKLQDCTMLVCGDDLVVICESVGTQEDAASLRA

SEQ ID NO. 64 (FR2, 1f)

STVTESDIRTEESIYQCCDLDPEARKAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYIKARAACRAAKLQDCSMLVCGDDLVVICEIEGXXEDPSXXXX

SEQ ID NO. 66 (FR16,1g)

MSTNPKPQRKTKRNINRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KARRSEGRSWAQPGYPWPLYGNEGMGWAGWLLSPHGSRPSWGPSDPRRRSRNLGKVIDTLTCGFAD LMGYIPLVGAPLGGVARALAQGFRDL

SEQ ID NO. 68 (FR16, 1q)

XXVTESDIRVEXSIYQCCDLAPEARVAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKAAAACRAAKLRECTMLVCGDDLVVICESAGVQEDAASXXX

SEQ ID NO. 70 (BNL3, 2e)

STVTERDIXTEESIYQACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRHCRASGVLTTSMGN TITCYIKALAACKAAGIVAPTMLVCGDDLVVISESQGVEEDDRNLXX

SEQ ID NO. 72 (FR4, 2f)

STVTERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVVISESQGAEEDERNLRV

SEQ ID NO. 74 (BNL5, 2h)

STVAERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVIISESQGTEEDERNLRV

SEQ ID NO. 76 (FR13,2k)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLXCRXPRXXXCATXKTXEQSQPRGRRQPIP KDRXTTGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHRSRNLGKVIDTLTXGFXD LMGYIPVVGAPVXGVARALAHGVRVLEDGINYETGNLPGCSFSISLLALLSITXPVSAVEIKNTXN TYMVTNDCSNXSITWQLXXAVLHVPGCVPCEREGNSSRCWIPVTPXVXVSRPGALTEGLRSHIDTI VASATFCSALYIGDVCGAIMIAAQVVIVSPEHHHFVQDCNCSIYPGHITGPRMX

SEQ ID NO. 78 (FR13, 2k)

STVTERDIRVEESVYLSCSLPEEARAAIHSLTERLYVGGPMQNSKGQSCGYRRCRASGVLTTSMGN TLTCYLKAQAACRAAGIVAPTMLVCGDDLVVISESQGTERDENNLRP



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Fig.30

SEQ ID NO. 80 (FR18,21)

STVTERDIRNEESIFLACSLPEEARTVIHSLTERLYIGGPMMNSKGQSCGYRRCRASGVFTTSMGN TITCYVKAMAACRAAGIDAPTMLVCGDDLVVISESQGTEEDFRNLRV

SEQ ID NO. 82 (PAK64,3q)

STVTEQDIRVEEEIYQCCDLEPEARRAIKSLTERLYVGGPMFNSKGLKCGYRRCRASGVLPTSYGN TITCYIKARAAARAGLQDPSFLVCGDDLVVVAESCXVDEEDRAALR

SEQ ID NO. 84 (BNL8, 4k)

STVTEKDIRPEEEVYQCCDLEPEARKVITALTERLYVGGPMHNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKASAAIRAAGLRDCTMLVCGDDLVVIAESDGVEEDNRALXA

SEQ ID NO. 86 (BNL12,41)

STVTEKDIRVEEEIYQCCDLXPEARKAISALTEXLYLGGPMYNSKGELCGYRRCRASGVYTTSFGN TVTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESEGVEEDSOPLRA

SEQ ID NO. 88 (EG81, 4m)

STVTERDIRVEEEVYQCCDLEPEARKAISALTERLYVGGPMFNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESDGVDEDRRALQA

SEQ ID NO. 90 (VN13,7a)

 ${\tt STVTERDVQTEHDIYQCCKLEPAARTAITSLTDRLYXGGPMXNSKGQACGYRRCRASGVLTTILAN\ TLTCYLKAQAACRAAGLKDFDMLVCGDDLVVISESLGVSEDTSALRA}$

SEQ ID NO. 92 (VN4,7c)

STVTERDIXTEHDIYQCCQLDPVARKAITSLTERLYCXGPMMNSRGQSCGYRRCRASGVLTTSLGN TLTCYLKAQAACRAAKLKNYDMLVCGDDLVVIAESGGVSEDVDALRA

SEQ ID NO. 94 (VN12,7d)

SSVTERDIRTEHDIYQCCQLDPVARKAITSLTERLYCGGPMYNSRGQSCGYRRCRASGVFTTSLGN TMTCYLKAQAACRAXKLKNFDMLVCGDDLVVIAESGGVPEDAGALRV

SEQ ID NO. 96 (FR1,9a)

STVTGRDIRTEXDIYLSCQLDPEARKAIKSLTERLYVGGPMYNSKGQLCGQRRCRASGVLPTSMGN TITCFLKATAACRAAGFTDYDMLVCGDDLVVVTESAGVNEDIANLRA

SEQ ID NO. 98 (NE98, 10a)

STVTEQDIRVELSIFQACDLKDEARRVITSLTERLYCGGPMFNSKGQHCGYRRCRASGVLPTSFGN TITCYIKAKAATKAAGIKNPSFLVCGDDLVVIAESAGIDEDKSALRA

SEQ ID NO. 100 (FR14,11a)

STVTERDIRTEESIYLSCQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRV



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Fig.3P

Figure 3 - continued

SEQ ID NO. 102 (FR15,11a)

STVTERDIRTEESIXXACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAXAACKXAGIVDPVMLVCGDDLVVISESKGVEEDQRDLXX

SEQ ID NO. 104 (FR19,11a)

 ${\tt MSTNPKPQRQTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRVGVRATRKTSERSQPRGRRQPIPKVRRTTGR}$

SEQ ID NO. 106 (FR19,11a)

STVTERDIRTEESXYLACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRX



Fig. 4A Core/El amino acid alignment



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o	HCV-1	BNL1	BNL2	CAM1078	FR2	FR16	HC-76	HC-J8	CH610	NE92	BNL3	FR4	FR13	EB 1	NZL1	HCV-TR	GB358	DK13	CAM600	GB809	HPCCOREEZA	HPCCOREZB	HPCCOREZC	GB724	BNL7	BE95	HK2	VN13	VN4	VN12	FR1	NE98	FRI9





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DK13	49		
CAM600	4 e		
GB809	4 e		
BNL7	4	28	
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Isolate	HCV1	HCV-J	BNL1	BNL2	CAM1078	FR2	FR16	HC-J6	HC-J8	CH610	NE92	BNL3	FR4	FR13	HCV-TR	GB116	DK13	CAM600	GB809	275	GB549	GB438	BNL7	BE95	HK2	VN13	VN4	VN12	FR1	NE98



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----I-T-V--AE-K-ISTG ----VE---ISSS ---S----IS--VE-K-TSTS VE-KDTGDS ---V-GL--K-TSSS ---V---V-XVE-K-TSQA ---V--I--K-NSHF HTST-X--V--V--V--------TSHS I---V--V--RS-S --S----/I-X-V--VEIK-TXNT LEW--TS--EHY--AS-I VHY--AS-V --VNY--AS-V IHY--AS-V ----GVNY--AS-V F---C--GLEYT-TS--V-S---YN---------T--VNY--AS-I EHY--AS-I VNY--AS-I ---VHYH-TS-I --011Y--IS-I ----OHY--AS-I VHYH-TS-] ---X--I----X-----I--

LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL -----AV---I -----A-G--------AV--------AV-----E----AV---I------AV----I --0-E-D. 116 118 220 24 26 76 32 33 34 36 36

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GB809-4 3B809-2

NE92 BNL3 FR4 BNL4 BNL5 BNL6 FR13 BR36 HCV-TR GB116 GB215 GB358 DK13 CAM600 CAMG27 GB549 GB438 BNL7 Isolate CAMG22 FR16 HC-J6 HC-J8 CH610 HCV-J BNL2 583







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34 44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
44 41 5a 7a 7c 7d 9a
BNL11 BNL12 BE95 BE100 HK2 VN4 VN12 FR1 NE98





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V3 VPC/VREGNASRCWVAMIPTVALTRDS-FLL-A-NN-SMXLL-VKXIIPLL-VKIIPVS-NVGEKVTIPVS-NVGEXI	ENSSGRFHIPIS-NIE-SRTFT-VS-NELQKIPVNEWKD-TIPVNQDT-TT-PVNQDT-TT-PVTTQ-STTVST	-LVQLSAFY -LVQLSAFY
V1 201 YHUTNDC PNS SIVYEAADAILHTPGCVPCKREGNASRCWVAMIT PTVAITRD S		
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10000000000000000000000000000000000000	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Isolate HCV-1 HCV-1 BNL1 BNL2 FR2 FR2 HC-J6 HC-J8 CH610 S83	BNL3 FR4 BNL4 BNL5 BNL6 FR13 BR36 HCVTR 24 GB809-4 GB809-4	GB215 GB358 DK13 CAM600 GB809-2 CAMG27 CAMG27 GB549 GB438 BNL7 BNL7 BNL8 BNL9 BNL10
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Fig. 46

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LAPI	ITDHHLAVS	AOI		LVDDR-T-	i	I	$\overline{\mathrm{L}}$	
40					7	48	42	52
41	4 ×	5a	5a	6 a	7c	7d	9a	10a
BNL12	GB724	BE95	BE100	HK2	VN4	VN12	FR1	NE98



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		31/74	
RRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFISP V	PGALTQGTMV-M	STI-AF	LNA-LESV-MGIVG
· · · · · ·	0 0 0 4 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0	• • • • •	
	a in in in in	11	3 3 3 3 8 8 8
Type la ld ld	8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	171 W W 女 女 母 母 女 女 . 1 X d U d d D O O O .	ひ 0 0 11 11 11 11 11 11 11 11 11 11 11 11
Isolate HCV-1 HCV-J BNL1 BNL2 FR2	HC-J6 HC-J8 CH610 S83 NE92 BNL3 BNL4 BNL5	FR13 BR36 HCVTR 24 GB809-4 Z1 GB116 GB215 GB358	DK13 CAM600 GB809-2 CAMG27 CAMG27 GB549 GB438 BNL7 BNL9 BNL9 BNL9



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			5	2/:	74			
GAMQ	GAMQ	AALMYRQ-A-	AALMYRQ-A-	A0A	LRM-QV	RMYEI	R-KY-OV	ALXG-SWRH-Q
GA	GA	AAL	AAL	T	GI		II	AI
LSA-LMSVVMAS	VDA-LESFVMAV	- 1	1 1	ASTGFVA-A-WSILA0	AST-V-GF-K-V-IMA-AFM	ASVSIRGV-E-VA-AFM	SSV-IHGFVA-AFM-I	PCAATAST-V-MM-XA
40					44	48	42	25
41	4 4	5a	5a	6а	7c	7d	9a	10a
BNL12	GB724	BE95	BE100	HK2	VN4	VN12	FR1	NE98

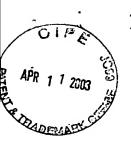


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310	OGENESTYPGHITGHRMA	0-1-0	j 1		V-DSXXX	L-	E0	V-EX	V-ER	V-D	V-E	V-EX	S-D	i	V-DX	TTS	V-TVS	L	DT	DVS	DAV	DAG	DAV	DT	DL	DA	ET		DQ	DV	D	A-D	D	D		V-D
SEQ	٠ ر		יע	œ	12						16																				30	32	34	36	38	40
Type	- P	1p	1d	1q] F	7.a	2p	7 0	ς 2	7 D	(1 ()	77 T	2g	2h	(1) 'X	3a	3p	4a	4 a	4 b	4 c	4 C	4 C	4 d	4 e	4 e	4 £	4 £	49	4 h		4 7	4 ×	4 7	4 k	41
Isolate	HCV-1	__	BNL1	BNL2	FR2	HC-J6	HC-J8	CH610	S83	NE92	BNL3	FR4	BNL4	BNL5	FR13	BR36	HCVTR	24	GB809-4	21	GB116	GB215	GB358	DK13	CAM600	GB809	CAMG22	CAMG27	GB549	GB438	BNL7	BNT8	g	$\overline{}$	BNL11	BNL12



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DT	V-NSN-V	S	-DT	1 1 1	-D	DXNX	17-7
•				44		42	
4×	5а	5а	6a	7c	7 d	g O	100



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									-	, ,	•								
7981	CTCCACAGTCACTGAGGGGGCATCCGTACGGAGGAGGCAATCTACCAAT	ATTT	CAGTTTT	TATGTCATA	!ACCRATT	:ATGTCATG-	AGCTTAAT-CA	TTTAT-C	TTGTCRTT	AA-GTT-CAT-GGG	ACGGAA-AAAAT-CATGG	GATAA-NTT-CAGG	AGTAA-ATT-CATGG	-G-GAA-GCT-CT-CTTG	AAA-AGTTAT-CG-TT-TG-	GGA-G-ATT-CA-TTGG	ACAGA-GGTAGAGA	ACATA-GAGA	ACAGTA-GGTAAA-AAA
7932	CTCCACAGTCA	AGAT-	NA	BL	GT	L9	AG	NA	NNNNNNN	AC	AC	9	ACA	BG-G-	A	A	A	T	II
SEQ ID				53	55	_	61					69	71	73	11	79			81
Туре	la	1p	1p	1d	1d	1d]e	1£	lg	2a	2 p	دع ه	2 f	2h	7, X,	21	3a A	3p	3g
Isolate	HCV−1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	$_{ m T1}$	T9	PAK64

Fig. 5A NS5B nucleotide alignment



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Isolate	Type	SEQ	
			7932
GB48	4 C		TACA-AGA-GGTCAG-G
GB116	4 C		-CA-AGA-GGTCA-G
GB215	4 C		-UB-DDGD-DDG-BD-DDG-B
GB358	4 C		
GB809	4 e		
GB549	4 q		-GCAGMA-GCB-BG
BNL8	4 , X	83	-ACA-AGA-GC-CA-AGG
BNL12	47	85	-GA-AGA-GGTCA-AG
EG81	4 m	87	-AC-AGGA-GGTCDGG
CHR18	5a		-CTCBCBTBARGTBT-T-TTTTTTTTT-
VN13	7a	68	
VN4	7c	91	``````````````````````````````````````
VN12	7d	93	T-CGC-TC-T
FR1	9a	95	G-G-G-C
NE98	\circ	97	
FR14	11a	66	-AAAT-C
FR15	_	101	-TAAAAAAA
FR19	11a	105	TAD



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,	8031										5	7/	74								
7982	TGACCTCGACCACA PACACACACA ACA A A CACACACA ACACA A CACACACA A CACACACA A CACACACACA A CACACACA A CACACACA A CACACACA A CACACACACA A CACACACACA A CACACACACA A CACACACACACA A CA			1-1-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-			7-C	A		-9-4	TC-T-GCC-GAGG-GA-ACTA-ACT				ATCEACC-IAI-A		AAAAAA	1 GCC GAGG GGACT-T	ATAGG-GA-	AG-GTGAAG	TGGG-GTA-ACGAAGA
ID					മ	55	57	61	63	6 3			69	71	73	77	79	1		,	⊒ Ω
]e												ת נו	5 G
	HCV-1	HCV-J	BE 90		BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	-	4 G	מאעם	£ 7770 4

Type SEQ

Isolate



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ברכמ הרכמ	- 1	-GG-GAGA	-GGAATAT-CCG	-GG-GAAA-T-CTG	-GG-GAATAAGCCG	-GGAATGATCCGA-	-GTAATTT-CCG	-GAAAA-AICCG	AAATCCG	TG-GGTAACGA	-GCAGACACAGTT-	GGTGAAATT-CATG	-TGGTAGAAA	GAAAA	-TA-GAGTGA-CT-	-C-AT-GCCTGAAG-GGAAATAGGA	C-AT-GCC-GAAG-GGAATAAGA	-AG
7982	1	-9	9	9	E	-CC	·9	9		CA-TGTT-GC-G	-CA-GT-GG-	-CCC-AT-	-CCC-AT-A-	9-DDDD	 	CC-AT-GC	CC-AT-GC	CC-AT-GC
SEQ	l I						83	85	87		89	91	93	95	97	66	0	103
Type	4°C	. 4c	4°C	4 C	4 e	4 g	4 ス	41	4 m	5a	7a	7c	7g	9a	0	\leftarrow	11a	\leftarrow
Isolate	GB48	ശ	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19



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											·										
	8032	AGGCTTTATGTGGGGGCCTTTTATGTGGGGGCCTTTATGTATG	CCC											コーチャーンり	らく - A.A 1	6C-A		GC-AA	GC-A	CGCA-CATCA-GTACAGT-ACTCC-G	1 0 H 0 F 0 C F 0 S S C C C C C C C C C C C C C C C C C
ഗ	ID				53	55	57	61	63	6 7										ć	p
Type	1	la	1b	1b	1q	1d	1d	1e	1£	1g	, p	3 p	2e	2£	2h	72 X	2]	e C	ر د د) (}	ر د
Isolate		HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	6L	77740	FOUTUR





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												61	/7	4							
5) 		8082	CTATCGCAGGTGCCGCGCGAGCGGCGTAPPPCAPAATAACTAACTAATAAAAAAAAAA									-)		9-180017	9.IVI>9V>	99IVII)0W		99.I.V			
	Type SEQ	ID		_						63				9	71	7	7	7			81
	\mathbf{T}_{λ}		1a	1 1 1 2	1b	1d	1 1 7	1d	le	1£	19	2a	7p	7 0	ŦZ	2h	2, X	21	3а	3p	3g
	Isolate		HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T 1	19	PAK64



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Q 8132 8132	CCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGCTT	ATT-GACTG	T-ATC-ATCT	GAT-GAA-G	AT-GAGG	AT-GAGG	CAA		AGCCG	AATG-GATTAG	A-GATAGDAG		-TTG-GATCDA	TP	5-QJ555-L	TG-GBBTTCA		ACTACT	A-A-G-	
SEC				53	55	57	61	63	6 3			69	71	73	77	79			81	
Type	la	1b	1b	1d	1d]q	1e	1£	1g	, c	2p	2e	2£	Zh	2k	21	3a	35	3g	
Isolate	HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64	





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								(64 <i>i</i>	74	ţ							
8137	9-	-GTCATCACTATCA	TCATCACATCA-G-	-GCATCACTATCA	-GATCA-G-	-GTTCGTTG	-GCATCATTAT-AG	TC-TACCTACCA-GTA	-CCACCTACCAGCG	-GAA	T-GAT-AGACATCG	-ATT-GA-AAGA-GAA-	AC-GT-AGTA-G-	AT-C-GAACCCTC	CTAAA	TAA	-AARTAAYT	<u>L</u>
SEQ	1										89	91	93	95	97	66	101	105
Type	4c	4c	4c	4c	4 e	49	4 7	41	4 m	5a	7a	7c	7d	9a	10a	11a	11a	11a
lsolate	GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FRI	NE98	FR14	FR15	FR19



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8182 CAGGACTGCACCATGCTCGTGTGGCGACGACTTAGTCGTTATCTGTGA GAACAC-T	
SEQ ID	53 55 61 63 77 73 81
Type 1a 1b	11 11 12 13 13 13 13 13 13 13 13 13 13 13 13 13
Isolate HCV-1 HCV-J	BE90 BNL1 BNL2 FR17 CAM1078 FR2 FR16 HC-J6 HC-J8 BNL3 FR4 BNL3 FR13 FR13 T1



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										_	U,	′ 7							
		TC70						~~~J~~~J~~~J~~~S~~~~~~~~~~~~~~~~~~~~~~					ATGAT-ACA	TIGAT-GCCAT-GA	T-ATGAT-GCCAT-G-T	TCCAT-AT-C-TCCAT	-CCGGTG	-W)	
	8182	AGA	ı	AGA	AGA	AT	A-A-GT	AGA	A-A	- 1	1	A	A-AA	A-AA	ACAT	A-AA-T	GTA(1	1
ഗ	ID							83	85	87		89	91	93	95	16	99	101	105
Type)	4 C	4 C	4c	4 C	4 e	49	4 7	41	4 m	5a	7а	7c	7d	9 a	10a	11a	11a	11a
Isolate		GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19



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AAGCGCGGGGTCCAGGAGGACGCGGCGAGCCTGAGAGCC --AAC---SEQ ID 53 57 61 63 69 71 73 77 81 Type FR17 CAM1078 Isolate FR2 FR16 HC-J6 HC-J8 BNL3



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		!	Fig.5N	
Isolate	Type	SEQ ID	8232	71
GB48	4 c	l I	ATCAGAAACGACC	
GB116	4 c		ATCAGAAACGAGCCG	
GB215	4 C		GATCAGAAACGAGCCGT-	
GB358	4 C) - -	
GB809	4 e		GGTCTGAAACGANCCGT	
GB549	4 q		GGCCAGTAAGAGCCC	
BNL8	4 사	83	GATCAGTAACCGAGCCCN	
BNL12	41	85	GACAGTT-CCAACCCC	
EG81	4 m	87	GATCGG-CCGCCGAGCCCAT	
CHR18	5a		GCAACGCTAAA	
VN13	7a	68	ragrecac	
VN4	7c	91	GT-GAATCTT-TT-ACGCCA	
VN12	7d	93	ı ı	
FR1	9a	95	GTTAA-CTATCT-AC	
NE98	Ö	97	AGCGC-T-	
FR14	4	66	1	
FR15	11a	101	CA-CGAGA	
FR19	$\overline{}$	105	AAGGCAACGAGAACNT-	

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09/74													
2694 STVTESDIRTEEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCG NSA-EQR	XSAXEK	- 五											
SEQ ID	554 662 67 77 70 80 80 80												
Type 1a 1b	ураванхуне dc bag fee dd у у у у у у у у у у у у у у у у у у	ת											
Isolate HCV-1 HCV-J	BNL1 BNL2 FR17 CAM1078 FR2 FR2 HC-J6 HC-J8 ARG8 NE92 BNL3 FR13 FR13 FR18 BR34 BR34												

Fig.6A NS5B amino acid alignment



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MHK-DLMHK-DLMHK-DLMHK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-DLMYK-QQMYK-QQMYK-QQMYK-QAMYK-QAMYK-QAMYK-QA
KVEVE-EKTAKVEVE-EKV-TA
88 886 1100 1102 1025
1054444460005444460000000000000000000000
GB48 GB116 GB215 GB358 GB358 GB809 CAMG22 GB549 GB438 CAR1/50 CAR1/50 CAR1/12 CAR1/12 EG81 BNL12 EG81 BE95 CHR18 VN13 VN13 VN13 VN13 FR14 FR14



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Fig.6C	2695	RASGVLTISCGNTLTCYIKARAACRAAGI,ODCTMI,VCGDDI,VVTC		1]] [-C =MM - M - M - M - M - M - M - M	7. 1. 1. N	X01IXI	· · · · · · · · · · · · · · · · · · ·		-1K	1	TVMTDAP			FTRROPDF	FTKNFUF		
U.	ID					56												78						α γ	
TVDA) 1 1	la	1b	1c	1q	1d	1q	1e	1£	1g	ר) מ י	3 p	20 20	2d	رع 4	7.£	2h	2 አ	21	3a	3a	3a	3b	30	ת ת
Tsolate	i i)	HCV-1	- Ē	2TY4	BNL1	BNL2	FR11	CAM1078	FR2	FR16	HC-J6	$\overline{}$	ARG8	NE92	BNL3	FR4	BNL5	FR13	FR18	BR34	BR36	BR33	T9	PAK64	



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72/14
88 88 99 100 100 100 100 100
050 100 050 050 050 050 050 050 050 050
GB48 GB116 GB215 GB358 GB358 GB358 CAMG22 GB438 CAR1/50 EG13 BNL8 BNL8 BNL12 EG13 UN13 VN13 VN13 VN13 FR1 FR1



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2745 2757	GVQEDAASLR	T	VT	N	NN	-XEV	-V-T	IE-XXPS		-Q-TEERN	-Q-NEERN	-Q-TEERN	1	-Q-AEERNV	-Q-TEERNV	-Q-TER-ENNP	-Q-TEERNV	i	ı	i	-CER-A	-CX-D-EDRAALR
SEQ ID								64						72								82
Type			1b	1q	1d	1q	1e	4 7	1g	رم م ر	2b	2q	2e	2.£	2h	2k	21	3a	3a	3a	3b	39
Isolate	HCV-1	\ \ \	BE90	BNL1	BNL2	FR17	CAM1078	FR2	R1	C-J		日9	BNL3	FR4	BNL5	FR13	FR18	R3	BR36	BR33	T9	PAK64
g.6E																						



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KRP- KRA- KRA-	-DEKRA-G- -GEKRX-G-	ERRA-	i i	-I-IDKQAT	EPXTX-P		ESQP	-DDRRA-Q-	H	TH	STS	VDA	-GPGAV	1	I	E	-KEORD-	——田——
								88			90	26	94	96	98	0	102	0
41 41 41 0 0 0	4, 4, O 0	4 £	4 4 ՄԱ	054	7	4 K	41	4 m	5а	5 а	7a	7c	7g	9a	$\overline{\mathbf{C}}$	11a	$\overline{}$	$\overline{\mathbf{H}}$
GB48 GB116 GB215	B35 B80	AMG	B54 B43	4	R1/5	\vdash	BNL12	EG81	BE95	CHR18	VN13	VN4	VN12	FR1	NE 98	FR14	FR15	FR19
1.6F																		